



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 122044**

**To: Mary Zeman**  
**Location: rem/2d61/2c70**  
**Art Unit: 1631**  
**Monday, May 17, 2004**

**Case Serial Number: 10/621401**

**From: Beverly Shears**  
**Location: Remsen Bldg.**  
**RM 1A54**  
**Phone: 571-272-2528**

**beverly.shears@uspto.gov**

### **Search Notes**

STIC-Biotech/ChemLib

122044

From: Zeman, Mary  
Sent: Friday, May 14, 2004 9:52 AM  
To: STIC-Biotech/ChemLib  
Subject: seq search

please search in 10/621401

Please run a regular search of SEQ ID NO: 145 in regular AND interference files

Please run an OLIGO search of SEQ ID NO: 145 in regular files.

Paper printout please

thank you

Mary K. Zeman  
Primary Examiner, 1631  
571-272-0723  
Remsen 2D61  
MAILBOX: REM 2C70  
mary.zeman@uspto.gov

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 5-17  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:35:53 ; Search time 60 Seconds  
(without alignments)  
913.570 Million cell updates/sec

Title: US-10-621-401-145

Perfect score: 1066

Sequence: 1 MKLASGFLVWLSLGGGLAQ.....PFMNSQRAACICAEKEKEL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1064	99.8	194	5	ABP62920	Human pol
2	1064	99.8	194	6	ADA57403	Human sec
3	1064	99.8	194	6	ADA56921	Human sec
4	1064	99.8	194	6	ADA41278	Human sec
5	1064	99.8	194	6	ADA40769	Human sec
6	1064	99.8	194	6	ABO13978	Novel hum
7	1064	99.8	194	6	ABR48024	Human sec
8	1064	99.8	194	6	ABR47739	Human sec
9	1064	99.8	195	2	AAV27572	Human sec
10	655.5	61.5	335	7	ADE08422	Novel pro
11	467	43.8	192	3	AAV82822	Murine TA
12	467	43.8	192	5	ABR08151	Murine GX
13	458	43.0	189	3	AAV88271	Human TAN
14	458	43.0	189	3	AAV87282	Human sig
15	458	43.0	189	4	AAE06607	Human pro
16	458	43.0	189	4	AAU12291	Human PRO
17	458	43.0	189	4	AAE88353	Human mem
18	458	43.0	189	4	AAE88353	Human mem
19	458	43.0	189	5	AAU36906	Human SPL
20	458	43.0	189	5	ABR08150	Human GXI
21	458	43.0	189	5	ABP64382	Human ORF
22	458	43.0	189	6	ABO17735	Novel hum
23	458	43.0	189	6	ABU80989	Human PRO
24	458	43.0	189	6	ABU66689	Human PRO
25	458	43.0	189	6	ABU59770	Novel sec

26	458	43.0	189	6	ABO24960	Human sec
27	458	43.0	189	6	ABU66965	Human sec
28	458	43.0	189	6	ADA45759	Novel hum
29	458	43.0	189	6	ADA76190	Human PRO
30	458	43.0	189	6	ADA18840	Human PRO
31	458	43.0	189	6	ADA61463	Homo sapi
32	458	43.0	189	6	ADB19248	Novel hum
33	458	43.0	189	6	ADB27789	Human PRO
34	458	43.0	189	6	ADA86268	Novel hum
35	458	43.0	189	6	ADB15832	Human PRO
36	458	43.0	189	6	ADA47618	Human PRO
37	458	43.0	189	6	ADA67413	Human PRO
38	458	43.0	189	6	ADB30420	Human PRO
39	458	43.0	189	6	ADA85716	Novel hum
40	458	43.0	189	6	ADA96928	Human PRO
41	458	43.0	189	6	ADA79232	Human PRO
42	458	43.0	189	6	ADA87371	Novel hum
43	458	43.0	189	6	ADB16573	Human PRO
44	458	43.0	189	6	ADA91665	Novel hum
45	458	43.0	189	6	ADB14728	Human PRO

## ALIGNMENTS

## RESULT 1

ABP62920

ID ABP62920 standard; protein; 194 AA.

AC ABP62920;

DT 14-OCT-2002 (first entry)

DE Human polypeptide SEQ ID NO 357.

KW Human; vulnery; dermatological; neuroprotective; nootropic; cancer;

KW antiparkinsonian; immunostimulant; cytosolic; immunosuppressive;

KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;

KW burn; central nervous system disorder; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease; immune disorder;

KW autoimmune disorder; multiple sclerosis; diabetes; allergy.

OS Homo sapiens.

XX WO200218424-A2.

XX PD 07-MAR-2002.

XX 31-AUG-2001; 2001WO-US027093.

XX 01-SEP-2000; 2000US-00654935.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;

XX Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;

XX WPI; 2002-583321/62.

XX N-PSDB; ABQ93399.

XX New polynucleotide and polypeptides, useful for treatment and diagnosis

XX of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral

XX sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple

XX Claim 20; SEQ ID NO 357; 284pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising one of

XX 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising

XX administering to a mammalian subject a composition comprising the protein

XX (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

XX (I), (II) and (III) are useful for diagnostic evaluation of disorders.

XX (I) is useful for gene therapy of diseases and (II) can be used for

CC therapeutic treatment. Diseases that may be treated include wound healing  
 CC and tissue repair, burns, central nervous system disorders (e.g.  
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral  
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple  
 CC sclerosis, diabetes and allergies. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 5; Length 194;  
 Best Local Similarity 99.5%; Pred. No. 3.9e-107;  
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60  
 DB 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60  
 QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 QY 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180  
 DB 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180  
 QY 181 RAACICAEKEEL 194  
 DB 181 RAACICAEKEEL 194

RESULT 2  
 ADA57403  
 ID ADA57403 standard; protein; 194 AA.

XX ADA57403;  
 AC ADA57403;  
 DT 20-NOV-2003 (first entry)  
 XX Human secreted protein #204.  
 DE  
 XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
 KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
 KW cardiovascular; antiarteriosclerotic; gene therapy;  
 KW human secreted protein; immune disorder; inflammation;  
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
 KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM;

PI WPI; 2003-167512/16.

DR N-PSDB; ADA56510.

XX New human secreted polypeptides and polynucleotides, useful for  
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory

PT conditions, respiratory disorders, cancers, CNS disorders, or  
 PT neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1596; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for  
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
 CC conditions, respiratory disorders, cancers, CNS disorders, or  
 CC neurodegenerative disorders, or polypeptides comprising an amino acid  
 CC sequence at least 95% identical to the new sequences. The polypeptides,  
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
 CC acids encoding the polypeptides, agonists or antagonists that binds to  
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
 CC compositions for diagnosing, treating or preventing an e.g. immune  
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
 CC polynucleotides are useful for chromosome identification, chromosome  
 CC mapping, for controlling gene expression through triple helix formation  
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
 CC from manure biological samples, in forensic biology, and as hybridization  
 CC probes. The polypeptides are useful for as molecular weight markers on  
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
 CC gels, to raise antibodies, for testing biological activities, and for  
 CC treating or preventing neural disorders, immune system disorders, and for  
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
 CC to one of the polypeptide of the invention. Note: The sequence data for  
 CC this patent did form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-107;  
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60  
 DB 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60  
 QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 QY 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180  
 DB 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180  
 QY 181 RAACICAEKEEL 194  
 DB 181 RAACICAEKEEL 194

RESULT 3

ADA56921

ID ADA56921 standard; protein; 194 AA.

XX ADA56921;

XX 20-NOV-2003 (first entry)

DT Human secreted protein #204.

DE

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
 KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
 KW cardiovascular; antiarteriosclerotic; gene therapy;  
 KW human secreted protein; immune disorder; inflammation;  
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;



inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
triple helix formation; antisense gene therapy; forensic biology.

OS Homo sapiens.  
XX WO2002102994-A2.  
XX 27-DEC-2002.  
XX 19-MAR-2002; 2002WO-US008278.  
XX 21-MAR-2001; 2001US-0277340P.  
XX 19-JUL-2001; 2001US-0306171P.  
XX 13-NOV-2001; 2001US-0331287P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM;  
XX WPI; 2003-167512/16.  
XX N-PSDB; ADA56025.  
XX New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.  
XX Claim 13; SEQ ID NO 1111; 1754pp; English.

The invention relates to 592 new human secreted polypeptides useful for  
diagnosing, treating or preventing e.g. immune disorders, inflammatory  
conditions, respiratory disorders, cancers, CNS disorders, or  
neurodegenerative disorders, or polypeptides comprising an amino acid  
sequence at least 95% identical to the new sequences. The polypeptides,  
antibodies or antibody fragments that bind to the polypeptides, nucleic  
acids encoding the polypeptides, agonists or antagonists that binds to  
the polypeptide, are useful in preparing diagnostic or pharmaceutical  
compositions for diagnosing, treating or preventing an e.g. immune  
disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
(e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
polynucleotides are useful for chromosome identification, chromosome  
mapping, for controlling gene expression through triple helix formation  
or antisense DNA or RNA, in gene therapy, for identifying individuals  
from minute biological samples, in forensic biology, and as hybridization  
probes. The polypeptides are useful for as molecular weight markers on  
sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
gels, to raise antibodies, for testing biological activities, and for  
treating or preventing neural disorders, immune system disorders,  
muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
renal, proliferative and/or cancerous diseases. This sequence corresponds  
to one of the polypeptide of the invention. Note: The sequence data for  
this patent did form part of the printed specification, but was obtained  
in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 194 AA;  
XX Query Match 99.8%; Score 1064; DB 6; Length 194;  
XX Best Local Similarity 99.5%; Pred. No. 3 9e-107;  
XX Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLASGFLVLMISLGGGLAQSDTSPTDESYSDWGLRHRLRGFSFVNSYFDSFLELLGK 60  
DB 1 MKLASGFLVLMISLGGGLAQSDTSPTDESYSDWGLRHRLRGFSFVNSYFDSFLELLGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCVD 120

Db 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCVD 120  
QY 121 TCGANKYRCDAKFRWCLXSIKSLKRSIGFYSKVEACDLSLVDVTVENTVWTLGCRPFMNSQ 180  
Db 121 TCGANKYRCDAKFRWCLXSIKSLKRSIGFYSKVEACDLSLVDVTVENTVWTLGCRPFMNSQ 180  
QY 181 RAACICAEKEEL 194  
Db 181 RAACICAEKEEL 194  
RESULT 4  
ADA41278  
ID ADA41278 standard; protein; 194 AA.  
XX AC ADA41278;  
XX 20-NOV-2003 (first entry)  
XX Human secreted protein.  
XX Human; secreted protein; cancer; hyperproliferative disorder;  
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;  
KW anaemia; allergic reaction; asthma; cardiovascular disorder;  
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;  
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;  
KW vulnery; cardiant; gene therapy.  
XX OS Homo sapiens.  
XX WO2002102993-A2.  
XX 27-DEC-2002.  
XX 19-MAR-2002; 2002WO-US008123.  
XX 21-MAR-2001; 2001US-0277340P.  
XX 19-JUL-2001; 2001US-0306171P.  
XX 13-NOV-2001; 2001US-0331287P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM;  
XX WPI; 2003-175238/17.  
XX New human secreted proteins and nucleic acid molecules, useful for  
PT preparing a diagnostic or pharmaceutical composition for diagnosing,  
PT preventing or treating cancer or other hyperproliferative disorder,  
PT asthma, allergies or AIDS.  
XX Claim 1; SEQ ID NO 1661; 3205pp; English.

The invention relates to novel genes ADA39629-ADA40565 and proteins  
ADA40566-ADA41501 for human secreted proteins, useful for preventing,  
treating or ameliorating medical conditions e.g. by protein or gene  
therapy. The polypeptides, nucleic acid molecules, antibodies or their  
fragments, and agonists or antagonists that bind to the polypeptide are  
useful for preparing a diagnostic or pharmaceutical composition for  
diagnosing or treating cancer or other hyperproliferative disorder. The  
polypeptides and nucleic acid molecules are also useful for detecting,  
preventing, diagnosing, prognosticating, treating or ameliorating cancer  
or other hyperproliferative disorders including neoplasms, autoimmune  
disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus  
erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic  
anaemia), haematopoietic or haematological disorders (e.g. anaemia,  
thrombocytopenia), allergic reactions including asthma or eczema,  
inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory  
bowel disease or Crohn's disease), neurodegenerative disorders (e.g.  
Alzheimer's disease or Parkinson's disease), cardiovascular disorders  
(e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,  
fungal or viral infections including HIV/AIDS), or wound healing and  
disorders of epithelial cell proliferation. The nucleic acids are also

CC useful for chromosome identification, radiation hybrid mapping or long-  
CC range restriction mapping, as molecular weight markers, or as  
CC hybridization or diagnostic probes. The polypeptides and antibodies are  
CC useful for providing immunological probes for differential identification  
CC of the tissues immunohistochemistry assays. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;  
Best Local Similarity 100.0%; Pred. No. 3.9e-107;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60  
DB 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGGSGYFLGLKVPESMDLGIPTMTKCCNQLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGGSGYFLGLKVPESMDLGIPTMTKCCNQLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXSCDLKRSLSGFVSKVEACDSLVDTVNTVTLGCRPFMNSQ 180  
DB 121 TCGANKYRCDAKFRWCLXSCDLKRSLSGFVSKVEACDSLVDTVNTVTLGCRPFMNSQ 180  
QY 181 RAACICAEKEEKEEL 194  
DB 181 RAACICAEKEEKEEL 194

RESULT 5  
ADA40769  
ID ADA40769 standard; protein; 194 AA.  
AC ADA40769;  
DT 20-NOV-2003 (first entry)  
XX Human secreted protein.  
DE Human; secreted protein; cancer; hyperproliferative disorder;  
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;  
KW anaemia; allergic reaction; asthma; cardiovascular disorder;  
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;  
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;  
KW vulnery; cardiant; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO2002102993-A2.  
XX  
PD 27-DEC-2002.  
XX  
XX 19-MAR-2002; 2002WO-US008123.  
XX  
XX 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
XX WPI; 2003-175238/17.  
XX  
XX New human secreted proteins and nucleic acid molecules, useful for  
PT preparing a diagnostic or pharmaceutical composition for diagnosing,  
PT preventing or treating cancer or other hyperproliferative disorder,  
PT asthma, allergies or AIDS.  
XX  
PS Claim 1; SEQ ID NO 1151; 3205pp; English.

XX  
CC The invention relates to novel genes ADA39629-ADA40565 and proteins  
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,  
CC treating or ameliorating medical conditions e.g. by protein or gene  
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their  
CC fragments, and agonists or antagonists that bind to the polypeptide are  
CC useful for preparing a diagnostic or pharmaceutical composition for  
CC diagnosing or treating cancer or other hyperproliferative disorder. The  
CC polypeptides and nucleic acid molecules are also useful for detecting,  
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer  
CC or other hyperproliferative disorders including neoplasms, autoimmune  
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus  
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic  
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,  
CC thrombocytopenia), allergic reactions including asthma or eczema,  
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory  
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.  
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders  
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,  
CC fungal or viral infections including HIV/AIDS), or wound healing and  
CC disorders of epithelial cell proliferation. The nucleic acids are also  
CC useful for chromosome identification, radiation hybrid mapping or long-  
CC range restriction mapping, as molecular weight markers, or as  
CC hybridization or diagnostic probes. The polypeptides and antibodies are  
CC useful for providing immunological probes for differential identification  
CC of the tissues immunohistochemistry assays. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;  
Best Local Similarity 99.5%; Pred. No. 3.9e-107;  
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60  
DB 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGGSGYFLGLKVPESMDLGIPTMTKCCNQLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGGSGYFLGLKVPESMDLGIPTMTKCCNQLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXSCDLKRSLSGFVSKVEACDSLVDTVNTVTLGCRPFMNSQ 180  
DB 121 TCGANKYRCDAKFRWCLXSCDLKRSLSGFVSKVEACDSLVDTVNTVTLGCRPFMNSQ 180  
QY 181 RAACICAEKEEKEEL 194  
DB 181 RAACICAEKEEKEEL 194

RESULT 6  
ABO13978  
ID ABO13978 standard; protein; 194 AA.  
XX  
XX ABO13978;  
XX  
XX 21-AUG-2003 (first entry)  
DT  
XX Novel human secreted protein #7.  
DE  
XX Human; secreted protein; cytostatic; neuroprotective; hepatotropic;  
KW gene therapy; cancer; liver disorder; hepatitis; neural disorder;  
KW Alzheimer's disease.  
XX  
XX Homo sapiens.  
OS  
XX US2003028003-A1.  
FN  
XX 06-FEB-2003.  
PD  
XX

PP	12-OCT-2001;	2001US-00974879.
XX	07-NOV-1997;	97US-0064900P.
PR	07-NOV-1997;	97US-0064908P.
PR	07-NOV-1997;	97US-0064911P.
PR	07-NOV-1997;	97US-0064912P.
PR	07-NOV-1997;	97US-0064983P.
PR	07-NOV-1997;	97US-0064984P.
PR	07-NOV-1997;	97US-0064985P.
PR	07-NOV-1997;	97US-0064987P.
PR	07-NOV-1997;	97US-0064988P.
PR	17-NOV-1997;	97US-0065089P.
PR	17-NOV-1997;	97US-0065090P.
PR	17-NOV-1997;	97US-0065094P.
PR	17-NOV-1997;	97US-0066095P.
PR	17-NOV-1997;	97US-0066100P.
PR	04-NOV-1998;	98NO-USO23433.
PR	05-MAY-1999;	99US-0305736.
PR	13-OCT-2000;	2000US-0239893P.
PR	08-MAR-2001;	2001US-0018683P.

XX	(ROSE//)	ROSEN C A.	
PA	(FENG//)	FENG P.	
PA	(RUBE//)	RUBEN S M.	
PA	(EBNE//)	EBNER R.	
PA	(OLSE//)	OLSEN H S.	
PA	(NIJU//)	NI J.	
PA	(WEIY//)	WEI Y.	
PA	(SOPP//)	SOPPET D R.	
PA	(MOOR//)	MOORE P A.	
PA	(KYAW//)	KYAW H.	
PA	(LAFI//)	LAFLEUR D W.	
PA	(SHIY//)	SHI Y.	
PA	(JANA//)	JANAT F.	
PA	(ENDR//)	ENDRESS G A.	
PA	(CART//)	CARTER K C.	
PA	(BIRS//)	BIRSE C E.	
XX			
PI	Rosen CA,	Feng P,	Ruben SM,
PI	Soppet DR,	Moore PA,	Kyaw H,
PI	Endress GA,	Carter KC,	Birse CE;
XX			
XX	WPI;	2003-479549/45.	
DR	N-PSDB;	ACD18865.	
XX			
PT	New nucleic acid molecule,	useful for preparing a medicament for	
PT	preventing, treating or ameliorating a medical condition e.g.,	can	
PT	liver disorders such as hepatitis or neural disorders such as Alz		
PT	disease.		

Qy	61	NGVCQRCRYGKAPKPRGKYPQEPNGCGSYFLGLKVPESMDLGIIPANTKCCNQLDVCYD	120
Db	61	NGVCQRCRYGKAPKPRGKYPQEPNGCGSYFLGLKVPESMDLGIIPANTKCCNQLDVCYD	120
Qy	121	TCGANKYRCDAKFWCLXKSCSDLKRLSLGKSVSKVEACDSLVDVTFVNTVTLGCRPPMNSQ	180
Db	121	TCGANKYRCDAKFWCLXKSCSDLKRLSLGKSVSKVEACDSLVDVTFVNTVTLGCRPPMNSQ	180
Qy	181	RAACICAEKEEKEEL	194
Db	181	RAACICAEKEEKEEL	194

RESULT 7  
ABR48024  
ID ABR48024 standard: protein: 194 AA.

XX	ABR48024;
AC	
XX	
DT	12-JUN-2003 (first entry)
XX	
XX	
DE	Human secreted protein, SEQ ID
XX	
XX	Cardiant; antiarrhythmic; ant
KW	vulneracy; antiinflammatory;
KW	antiparkinsonian; gene therapy
XX	
OS	Homo sapiens.
XX	
PN	WO200295010-A2.
XX	
PD	28-NOV-2002.
XX	
PF	19-MAR-2002; 2002WO-US009785.
XX	
PR	21-MAR-2001; 2001US-0277340P.
PR	19-JUL-2001; 2001US-030617P.
PR	13-NOV-2001; 2001US-0331287P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA. Ruben SM:

XX  
DR WPI: 2003-129429/12.

XX	Novel human secreted proteins, useful for detecting, preventing,
PT	diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT	disorders such as arrhythmia.

PS Claim 13: SEO ID NO 915: 1881pp: English.

The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins ABR48145 and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in

CC electronic format and is available from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ

Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;  
Best Local Similarity 100.0%; Pred. No. 3.9e-107;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFVSNSYFDSFLELLGGK 60  
Db 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFVSNSYFDSFLELLGGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120  
Db 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTNTVTLGCRPFMNSQ 180  
Db 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTNTVTLGCRPFMNSQ 180  
QY 181 RAACICAEKEEKEEL 194  
Db 181 RAACICAEKEEKEEL 194

## RESULT 8

ID ABR47739 standard; protein; 194 AA.

AC ABR47739;

DT 12-JUN-2003 (first entry)

XX Human secreted protein, SEQ ID 630.

DE Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;  
KW vulnerable; antiinflammatory; nootropic; neuroprotective;  
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.

OS Homo sapiens.

FN WO200295010-A2.

XX 28-NOV-2002.

PF 19-MAR-2002; 2002WO-US009785.

XX 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

DR Novel human secreted proteins, useful for detecting, preventing,  
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular  
PT disorders such as arrhythmia.

XX Claim 13; SEQ ID NO 630; 1881pp; English.

ES The present invention relates to novel human secreted proteins (ABR47633-  
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins  
CC and their coding sequences are useful for the preparation of a diagnostic  
CC or pharmaceutical composition for diagnosing or treating a cardiovascular  
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary  
CC arteriosclerosis and myocardial ischemia), neural disorders, immune  
CC system disorders, muscular disorders, reproductive disorders,  
CC gastrointestinal disorders, pulmonary disorders, renal disorders, for  
CC proliferative disorders and/or cancerous diseases and conditions, for

CC wound healing and epithelial cell proliferation, to treat inflammation or  
CC infection, for treating thrombosis and arteriosclerosis, for treating or  
CC preventing neural damage which occurs in neuronal disorders or  
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
CC disease, to enhance bone and periodontal regeneration and aid in tissue  
CC transplants or bone grafts, to prevent skin aging or hair loss, to  
CC stimulate growth and differentiation of haematopoietic cells and bone  
CC marrow cells when used in combination with other cytokines, to maintain  
CC organs before transplantation or for supporting cell culture of primary  
CC tissues, to increase or decrease differentiation or proliferation of  
CC embryonic stem cells, or to modulate mammalian characteristics or  
CC metabolism. Note: The sequence data for this patent was published in  
CC electronic format and is available from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ

Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;  
Best Local Similarity 99.5%; Pred. No. 3.9e-107;  
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFVSNSYFDSFLELLGGK 60  
Db 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSGFVSNSYFDSFLELLGGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120  
Db 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTNTVTLGCRPFMNSQ 180  
Db 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTNTVTLGCRPFMNSQ 180  
QY 181 RAACICAEKEEKEEL 194  
Db 181 RAACICAEKEEKEEL 194

## RESULT 9

AAAY27572  
ID AAY27572 standard; protein; 195 AA.

XX AC  
XX AAY27572;

XX 30-JUL-1999 (first entry)

XX Human secreted protein encoded by gene No. 6.

DE Human; secreted protein; fusion protein; gene therapy; protein therapy;  
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX WO9924836-A1.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US023435.

XX 07-NOV-1997; 97US-0064900P.

PR 07-NOV-1997; 97US-0064908P.

PR 07-NOV-1997; 97US-0064911P.

PR 07-NOV-1997; 97US-0064912P.

PR 07-NOV-1997; 97US-0064983P.

PR 07-NOV-1997; 97US-0064984P.

PR 07-NOV-1997; 97US-0064985P.

PR 07-NOV-1997; 97US-0064987P.

PR 07-NOV-1997; 97US-0064988P.  
PR 17-NOV-1997; 97US-0066089P.  
PR 17-NOV-1997; 97US-0066090P.  
PR 17-NOV-1997; 97US-0066094P.  
PR 17-NOV-1997; 97US-0066095P.  
PR 17-NOV-1997; 97US-0066100P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Feng P, Carter KC, Endress GA, Rosen CA, Ruben SM, Janat F;  
PI Ni J, Wei Y, Moore PA, Soppet DR, Kyaw H, Lafleur DW, Olsen HS;  
PI Shi Y, Ebner R;  
XX  
XX WPI; 1999-337740/28.  
DR N-PSDB; AAX84938.  
XX  
XX New human secreted proteins and coding sequences useful for treating  
PT disorders of the immune system and hyperproliferative disorders.  
XX  
XX Claim 11; Page 352-353; 507pp; English.  
XX  
XX This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX84924) for increasing the stability of the fused protein  
CC as compared to the human protein only. The invention relates to 125 novel  
CC genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino  
CC acid sequences AAX27567-Y27933) which are useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,  
CC pathological conditions can be diagnosed by determining the amount of the  
CC new polypeptides in a sample or by determining the presence of mutations  
CC in the new polynucleotides. Specific uses are described for each of the  
CC 125 polynucleotides, based on which tissues they are most highly  
CC expressed in (see AAX84933 for described uses)  
XX  
XX Sequence 195 AA;  
SQ

Query Match 99.8%; Score 1064; DB 2; Length 195;  
Best Local Similarity 100.0%; Pred. No. 3.9e-107;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60  
DB |||||  
1 MKLASGFLVWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60  
QY |||||  
61 NGVCQYRCRYGKAPMPRGYKQBPNGCGSYFGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
DB |||||  
61 NGVCQYRCRYGKAPMPRGYKQBPNGCGSYFGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
QY |||||  
121 TCANKYRCDAKFRWCLXSCSLKRSGLGFVSKVEACDSLVDVTFNTVMTLGCRTFMNSQ 180  
DB |||||  
121 TCANKYRCDAKFRWCLXSCSLKRSGLGFVSKVEACDSLVDVTFNTVMTLGCRTFMNSQ 180  
QY |||||  
181 RAACICAEKEEL 194  
DB |||||  
181 RAACICAEKEEL 194

RESULT 10  
ADE08422  
ID ADE08422 standard; protein; 335 AA.  
XX  
XX ADE08422;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Novel protein (useful for identifying genetic disorders) #577.  
DE  
XX  
XX novel gene; novel protein; tissue marker; molecular weight marker;  
KW chromosome marker; genetic disorder.  
XX  
XX Unidentified.  
OS  
XX

PN WO2003054152-A2.  
XX  
XX 03-JUL-2003.  
XX  
XX 10-DEC-2002; 2002WO-US039555.  
PF  
XX  
XX 10-DEC-2001; 2001US-0339739P.  
PR  
XX 11-DEC-2001; 2001US-0339453P.  
PR  
XX 14-MAR-2002; 2002US-0365091P.  
PR  
XX 14-MAR-2002; 2002US-0365384P.  
PR  
XX 12-APR-2002; 2002US-0372381P.  
PR  
XX 12-APR-2002; 2002US-0372615P.  
PR  
XX 22-APR-2002; 2002US-00128558.  
PR  
XX 24-APR-2002; 2002US-0376045P.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
XX  
XX WPI: 2003-569235/53.  
DR N-PSDB; ADE07511.  
DR  
XX  
XX New polynucleotides, useful for expressing recombinant proteins for  
PT analysis, characterization or therapeutic use, or as markers for tissues  
PT in which the corresponding protein is preferentially expressed.  
XX  
XX Claim 20; SEQ ID NO 1488; 1177pp; English.  
PS  
XX  
XX The invention comprises the amino acid and coding sequences of novel  
CC proteins. The DNA and protein sequences of the invention are useful as:  
CC markers for tissues in which the corresponding protein is preferentially  
CC expressed; as molecular weight markers on gels; as chromosome markers or  
CC tags; to identify chromosomes or to map related gene positions; and to  
CC compare with endogenous DNA sequences in patients to identify potential  
CC genetic disorders. The present amino acid sequence represents a protein  
CC of the invention.  
XX  
XX Sequence 335 AA;  
SQ

Query Match 61.5%; Score 655.5; DB 7; Length 335;  
Best Local Similarity 60.5%; Pred. No. 1.9e-62;  
Matches 133; Conservative 6; Mismatches 16; Indels 65; Gaps 3;

QY 1 MKLASGFLVWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60  
DB |||||  
1 MKLASGFLVWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60  
QY |||||  
61 NGVCQYRCRYG-----KAPMPRGYKQBPNGCGSYF--LGLKVPE----- 99  
DB |||||  
61 NGVCQYRCRYGCAVSLSVKTVAGGMDSPREVTICLALFPVTHLEPLDLADKNQNSIKR 120  
QY |||||  
100 -----SMDLGIPTAMTKCCNQL 115  
DB |||||  
121 LKQILVAEFLAGGSGQQQLGKKSKWFESHYSVTSSSSSPDLMDLGIPTAMTKCCNQL 180  
QY |||||  
116 DVCYDTCGANKYRCDAKFRWCLXSCSLKRSGLGFVSKVE 155  
DB |||||  
181 DVCYDTCGANKYRCDAKFRWCLXSCSLKRSGLGFVSKVE 220

RESULT 11  
AAY88282  
ID AAY88282 standard; protein; 192 AA.  
XX  
XX AAY88282;  
AC  
XX  
XX 16-OCT-2000 (first entry)  
DT  
XX  
XX Murine TANGO 180 protein.  
DE  
XX  
XX TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185;  
KW

KW TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine;  
KW secreted protein; transmembrane protein; gene therapy; vaccine;  
KW diagnosis; treatment; detection.  
XX  
OS Mus sp.  
PN WO200018904-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 30-SEP-1999; 99WO-US022817.  
XX  
PR 30-SEP-1998; 98US-00164220.  
XX  
PR 02-OCT-1998; 98US-00164169.  
XX  
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
PA Barnes TM;  
PI  
XX WPI: 2000-293144/25.  
XX  
DR N-PSDB; AAA39955, AAA39956.  
XX  
XX Isolated nucleic acids encoding TANGO polypeptides useful for preventing,  
PT diagnosing and treating diseases associated with inappropriate protein  
PT expression.  
XX  
XX Claim 9; Fig 2; 249pp; English.  
PS  
XX This invention describes novel human and murine nucleic acids encoding  
CC TANGO polypeptides (which are either wholly secreted or transmembrane  
CC proteins) which can be used for gene therapy and/or vaccination. The  
CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic  
CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215  
CC polypeptides according to standard recombinant DNA methodologies. They  
CC may also be used to detect and quantify the presence of TANGO nucleic  
CC acids in a sample and therefore identify or diagnose diseases associated  
CC with inappropriate TANGO expression (e.g. diseases related to over or  
CC under expression of the polypeptides or the expression of inactive  
CC polypeptides). The nucleic acids and the polypeptides they encode may be  
CC used according to standard gene therapy protocols, to treat diseases  
CC associated with inappropriate TANGO expression by supplementing a  
CC patient's own production of the polypeptide or to rectify mutations that  
CC may result in expression of an abnormally active polypeptide. The  
CC polypeptides may also be used to identify and produce agonists and  
CC antagonists of TANGO expression and activity which may be used to  
CC modulate TANGO related processes and diseases. The polypeptides are  
CC particularly useful for use as antigens for producing antibodies to TANGO  
CC proteins which may be used for inhibiting the activity of TANGO proteins.  
CC They may also be used to detect and quantify the presence of TANGO  
CC proteins in samples and therefore identify patients in whom the protein  
CC is over- or under-expressed. This sequence represents the murine TANGO  
CC 180 protein described in the method of the invention  
XX  
SQ Sequence 192 AA;  
Query Match 43.8%; Score 467; DB 3; Length 192;  
Best Local Similarity 43.9%; Pred. No. 2.9e-42;  
Matches 83; Conservative 43; Mismatches 49; Indels 14; Gaps 3;  
QY 8 LVNLWSLGGGLAQSDTSPTDESYDW-GLRHLSGFESVNSYFSLFLGGKNGVCQ 65  
DB 16 LLLLTATARGQDQQT-----TDWRATLKTIRNGIHKIDTYLNAALDLGGEDGLCQ 67  
QY 66 YRCRYGKAMPRGYKPPQPNCGSGYFLGLKVPESMDLGIPTAMTKCNOLDVCYDFCGAN 125  
DB 68 YKSDGSKVPFRGYKPPQPNCGSGYFLGV-----HLNIGIPSLTKCNQHDRCYETCGKS 123  
QY 126 KYRCDKAFRWCLXISDKRLSGFYSKVACDLSLDTVNTVTLGCRPFMNSQRAACI 185  
DB 124 KNDCEEFQYCLSKICRDVQKTLGLSQNVQACETTVELLFDPSVHLGCKPFLDYSQRAACW 183  
QY 186 CAEEKEEL 194  
| | | | |

DB 184 CRYEKTDL 192  
RESULT 12  
ABB08151  
ID ABB08151 standard; protein; 192 AA.  
XX  
AC ABB08151;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Murine GXII PLA2 (mGXII-1 PLA2) polypeptide.  
XX  
KW Phospholipase A2; GXII PLA2; phosphatidylethanolamine; Th2; GV PLA2;  
KW transgenic; immunosuppressive; antiallergic; cytostatic; antimicrobial;  
KW antidiabetic; antirheumatic; antiarthritic; antiinflammatory; mouse;  
KW neuroprotective; cerebroprotective; antiinfertility; contraceptive;  
KW mGXII-1 PLA2; enzyme.  
XX  
OS Mus musculus.  
XX  
PN WO200240655-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 06-NOV-2001; 2001WO-US044125.  
XX  
PR 06-NOV-2000; 2000US-0246316P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
PI Ho I, Arm JP, Austen KF, Glimcher LH;  
XX  
DR WPI: 2002-500219/53.  
XX  
N-PSDB; ABL69856.  
XX  
XX New group XII phospholipase A2 protein, useful for identifying modulators  
PT used for modulating prostaglandin production by Th2 cell and Th2 cell  
PT differentiation/activity, and treating allergy, cancer and type I  
PT diabetes.  
XX  
PS Claim 17; Page 73-74; 77pp; English.  
XX  
CC The invention relates to an isolated group XII phospholipase A2 (GXII  
CC PLA2) protein or its biologically active portion, where the protein  
CC selectively hydrolyses arachidonic acid in sn-2 position of  
CC phosphatidylethanolamine. Methods of modulating Th2 cell differentiation  
CC activity by modulating either GXII PLA2 or GV PLA2 which is also  
CC preferentially expressed in T cells are provided. The GXII PLA2 proteins  
CC can be used to prepare anti-GXII PLA2 antibodies. The GXII PLA2 encoding  
CC nucleic acid molecules can be used to prepare non-human transgenic  
CC animals that contain cells carrying a transgene encoding GXII PLA2  
CC protein or a portion of GXII PLA2 protein. Prostaglandin production can  
CC be increased by stimulators of GXII PLA2 or GV PLA2 which is further  
CC useful for prolonging survival of the graft and thus has applications in  
CC bone marrow transplantation or solid organ transplantation, and for  
CC increasing production of Th2-promoting cytokines for commercial purposes.  
CC Modulating the type of T helper cell response mounted in the individual  
CC suffering from the disease condition e.g., inhibition of Th2 cell  
CC response using GXII PLA2 or GV PLA2 inhibitors is carried out for  
CC inhibiting prostaglandin production to thereby inhibit production of Th2-  
CC associated cytokines in: (a) allergic patients to downregulate production  
CC of pathogenic IGE antibodies; (b) cancer patients; and (c) subjects with  
CC infectious diseases. Stimulation of Th2 cell response using GXII PLA2 or  
CC GV PLA2 stimulators is useful for treating autoimmune diseases associated  
CC with Th2-type dysfunction, such as type I diabetes, rheumatoid arthritis,  
CC etc. The methods provided are also useful in treating conditions such as  
CC inflammation, arthritis, multiple sclerosis, stroke, infertility, and  
CC also have contraceptive uses. The present sequence represents the mouse  
CC GXII PLA2 (mGXII-1 PLA2)  
XX  
SQ Sequence 192 AA;









QY 126 KYRCDKFWCLXSICSDLKRSIGFVSKVEACDSLVDVTWTLGCRPFMNSQRAACI 185  
Db 121 KNDCEBFQYCLSKICRDVQKTIGLTQHVQACETTVELLFDVSIHLGCKPYLDSQRAACR 180  
QY 186 CAERKEEL 194  
Db 181 CHYEKTDL 189

Search completed: May 17, 2004, 10:42:16  
Job time : 62 secs



```

; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-175

Query Match      34.4%; Score 367; DB 4; Length 123;
Best Local Similarity 50.0%; Pred. No. 2.6e-34;
Matches 62; Conservative 27; Mismatches 31; Indels 4; Gaps 1;

QY 71 GKAMPREGYKQBPNGGSGYFLGLKVPESMDLGPAMTKCCNOLDVCYDTCGANKYRCD 130
DB 4 GSKPPRRYGYRPSPPNGGSGFLGV-----HLNIGIPSLTKCCNQHDCRYETCGKSKNDCD 59
QY 131 AKFRWCLXISCDLKRSLGFSKVEACDSLVDTVNTVTLGCRPFPMNSQRAACICAE 190
DB 60 EEFQYCLSKICRDVQKTLGLTQHVOACETTVELLFDVSLHGLCKPYLDSQRAACRCHYEE 119
QY 191 KEEL 194
DB 120 KTDL 123

RESULT 4
US-08-485-449-6
; Sequence 6, Application US/08485449
; Patent No. 5824789
; GENERAL INFORMATION:
; APPLICANT: VANDENBERG, DAVID
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,449
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KONSKE, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20296-20035.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-449-6

Query Match      7.9%; Score 84.5; DB 2; Length 389;
Best Local Similarity 22.0%; Pred. No. 0.27;
Matches 29; Conservative 15; Mismatches 41; Indels 47; Gaps 5;

QY 59 GKNVQCYRCRYGKAPMPR-----PGYKQBPNGGSGY 91
DB 251 GTSGSQFKTCWRAAEFFRAIGAALRERLSRAIFIDTHNRNSGAFQPLRPRRLSGELVY 310
QY 92 FLGLKVPESMD-----LGIPAMT-KCCNOLDVCYDTCGA-----NKYRCDAKF 133
```

Db 311 F--EKSPDFCERDPTLGLSPGTRGRACNKTSLRLDGGSLCCGRGHNVLRQTRVERCHCRF 368  
QY 134 RWCLXSICDLK 145  
Db 369 HWCYVLCDECK 380

RESULT 5  
US-08-833-963C-2  
; Sequence 2, Application US/08833963C  
; Patent No. 5916769  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, et al.  
; TITLE OF INVENTION: Extracellular/Epidermal Growth Factor  
; TITLE OF INVENTION: HCAR58X  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Ave  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,963C  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US96/05033  
; FILING DATE: 10-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PP258  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 443 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-833-963C-2

Query Match 7.8%; Score 83.5; DB 2; Length 443;  
Best Local Similarity 21.8%; Pred. No. 0.42;  
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;  
QY 6 GFLVW-----LSLGGGLAQSPTSPTDEESYSD---W--GLRHRL-----GSP 43  
Db 10 GSLLLWALLLLGLGASPDSEEDSYCTDGYEWDPSQCHRDVNECLTPEACKGEM 69  
QY 44 ESNVSYFDSFLELLGGKNGVCQYRC-----RYGKAMP-----RPGYKP 82  
Db 70 KCINHY-----GG-----YLCLPSAAVINDLHGEPPPPVPPAQPHPNCPGYP 115  
QY 83 QEPNGCGSYFLGLKVPESMDLGPAMTKC-----CNQLDVCYDTGANKYR-----C--- 129  
Db 116 DDQSC-----VDVDECAQALHDCRPSQDCHNLPGSYQCTCPGYRKIGPECVDI 165  
QY 130 -DAKFRWCLXSICDLKSL-----GF-----VSKVEACD---SLVDTVFNVTWL 171  
Db 166 DECRYRYCQHR-CVNLPGSFRQCCEPGFQLGNPNRSCVDVNECDMGAPCEQRCFNSYGT 224  
QY 172 GCR 174  
|||

Db 225 LCR 227  
RESULT 6  
US-08-980-514-1  
; Sequence 1, Application US/08980514  
; Patent No. 6004753  
; GENERAL INFORMATION:  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT  
; TITLE OF INVENTION: EIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/980,514  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0436 US  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 443 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRSTNOT13  
; CLONE: 2786449  
US-08-980-514-1

Query Match 7.8%; Score 83.5; DB 3; Length 443;  
Best Local Similarity 21.8%; Pred. No. 0.42;  
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;  
QY 6 GFLVW-----LSLGGGLAQSPTSPTDEESYSD---W--GLRHRL-----GSP 43  
Db 10 GSLLLWALLLLGLGASPDSEEDSYCTDGYEWDPSQCHRDVNECLTPEACKGEM 69  
QY 44 ESNVSYFDSFLELLGGKNGVCQYRC-----RYGKAMP-----RPGYKP 82  
Db 70 KCINHY-----GG-----YLCLPSAAVINDLHGEPPPPVPPAQPHPNCPGYP 115  
QY 83 QEPNGCGSYFLGLKVPESMDLGPAMTKC-----CNQLDVCYDTGANKYR-----C--- 129  
Db 116 DDQSC-----VDVDECAQALHDCRPSQDCHNLPGSYQCTCPGYRKIGPECVDI 165  
QY 130 -DAKFRWCLXSICDLKSL-----GF-----VSKVEACD---SLVDTVFNVTWL 171  
Db 166 DECRYRYCQHR-CVNLPGSFRQCCEPGFQLGNPNRSCVDVNECDMGAPCEQRCFNSYGT 224  
QY 172 GCR 174  
|||

## RESULT 7

US-08-485-449-2  
; Sequence 2, Application US/08485449  
; Patent No. 5824789

## GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID  
TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE  
SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 7

## CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA

ZIP: 94304-1018

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,449

## FILING DATE:

CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 20296-20035.00  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 389 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-449-2

Query Match 7.7%; Score 82.5; DB 2; Length 389;  
Best Local Similarity 21.2%; Pred. No. 0.46;  
Matches 28; Conservative 16; Mismatches 41; Indels 47; Gaps 5;

QY 59 GKNGVCQYRCRYGKAPMPR-----PGYKQPEPNGCGSY 91

Db 251 GTSGSCQFKTCWRAAPEFRAVGAALRRLGRLAIFDTHNRNSGAFQPLRPRLSGELVY 310

QY 92 FLGLKVPESMD----LGIPAMT-KCNQLDVCYDTGCA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTMGSPGTRGRACNKTSLRLDGGSLCCGRHNVLRQTRVERCHCRF 368

QY 134 RWCLXSICSLDK 145

Db 369 HWCCYVLCDECK 380

## RESULT 8

US-08-485-449-7  
; Sequence 7, Application US/08485449  
; Patent No. 5824789

## GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID  
TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE  
SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 7

## CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,449

## FILING DATE:

CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 20296-20035.00  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

## INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 389 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-485-449-7

Query Match 7.7%; Score 82.5; DB 2; Length 389;

Best Local Similarity 21.2%; Pred. No. 0.46;

Matches 28; Conservative 16; Mismatches 41; Indels 47; Gaps 5;

QY 59 GKNGVCQYRCRYGKAPMPR-----PGYKQPEPNGCGSY 91

Db 251 GTSGSCQFKTCWRAAPEFRAVGAALRRLGRLAIFDTHNRNSGAFQPLRPRLSGELVY 310

QY 92 FLGLKVPESMD----LGIPAMT-KCNQLDVCYDTGCA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTMGSPGTRGRACNKTSLRLDGGSLCCGRHNVLRQTRVERCHCRF 368

QY 134 RWCLXSICSLDK 145

Db 369 HWCCYVLCDECK 380

## RESULT 9

US-08-485-449-5

; Sequence 5, Application US/08485449

; Patent No. 5824789

## GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID

TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE

SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,449

FILING DATE:

CLASSIFICATION: 536

```

; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20296-20035.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-449-5

Query Match 7.6%; Score 81; DB 2; Length 376;
Best Local Similarity 21.7%; Pred. No. 0.66;
Matches 28; Conservative 15; Mismatches 42; Indels 44; Gaps 5;

Qy 59 GKNGVCVRCRYGKAPMR-----PGYKPOEPNGCGSYFL 93
Db 241 GTSGSCGFKTCWRAPPEFRAGAALRLRLAIFITHNNSGAFQRLRPRLSGLYVF- 299
Qy 94 GLKVPESMD---LGIPAMT-KCCNQLDVCYDTGCA-----NKYRCDAPKFWC 136
Db 300 -EKSPDFCFERDPTGSPGTRGRACNKTSLRLDGGSLCCGRGHNVLRQTRVRCRCHRFHWC 358
Qy 137 LXSTCSDLK 145
Db 359 CYVLCDECK 367

RESULT 10
US-09-482-273-201
; Sequence 201, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030FI
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 201
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-482-273-201

Query Match 7.4%; Score 79; DB 4; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.018;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 108 MTKCCNQLDVCYDTGCG 123
Db 1 LTKCCNQHDRCYETCG 16

RESULT 11
US-09-252-991A-21977
; Sequence 21977, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21977
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-21977

Query Match 7.4%; Score 79; DB 4; Length 219;
Best Local Similarity 26.1%; Pred. No. 0.55;
Matches 30; Conservative 13; Mismatches 44; Indels 28; Gaps 5;

Qy 67 RCRYGKAPMRPGYKPOEPNGCGSYFLG-----LKVPEMDLG 104
Db 10 RSRPSWAPWAPG--AEKPMGCWREFFGRSADRGRYFKGBEILACHEAGITVFVKLTSG 67
Qy 105 IPAMTKCCNQLDVCYDTGCGANKYRCD--KFRWCLXISCDLKSGLGFSVKVEAC 157
Db 68 ATAAGR-FGKGDFIYD-AAXNEYRCAPQSLIWRFSVEKGLKLRVYSSHCQCG 120

RESULT 12
US-08-185-432-16
; Sequence 16, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
```

US-08-185-432-16

Query Match 7.3%; Score 77.5; DB 1; Length 2471;  
Best Local Similarity 23.6%; Pred. No. 19;  
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;

QY 63 VCOY-----RCRYGKAPMPRP-GYKQEPNGCGSYFLGLKVPESMDL-----103  
DB 528 VQCIDIDDCSSTPCINGAKCIDHPNGYEQ-----CATGFTGVLCEENIDNCDDPPCHHGQ 583

QY 104 ---GIPAMTKCCN-----QLDVCYDTGANKYRC-----129  
DB 584 CQGDIDSYTCINPGYMGALCSQDIDECYSSPCINDGRCDLVNGYQCNCQPGTGVNCE 643

QY 130 ----DAKFRWCLXSICSD-LKR-----SLGFVSKVEACDSDLVDTVFNVTWTLG--CRPFM 177  
DB 644 INFDDCASNPCHIGICMDGINRYSCVSPGFTG--QRCNIDIDECASNPCKRGATCINGV 701

QY 178 NSORAAICAE 188  
DB 702 NGFR--CICPE 710

## RESULT 13

US-08-083-590A-19  
; Sequence 19, Application US/08083590A  
; Patent No. 5786158  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, S. et al.  
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods  
; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And  
; TITLE OF INVENTION: Nucleic Acids  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/083.590A  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 8698864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2471 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-083-590A-19

Query Match 7.3%; Score 77.5; DB 1; Length 2471;  
Best Local Similarity 23.6%; Pred. No. 19;  
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;

QY 63 VCOY-----RCRYGKAPMPRP-GYKQEPNGCGSYFLGLKVPESMDL-----103  
DB 528 VQCIDIDDCSSTPCINGAKCIDHPNGYEQ-----CATGFTGVLCEENIDNCDDPPCHHGQ 583

QY 104 ---GIPAMTKCCN-----QLDVCYDTGANKYRC-----129  
DB 584 CQGDIDSYTCINPGYMGALCSQDIDECYSSPCINDGRCDLVNGYQCNCQPGTGVNCE 643

QY 130 ----DAKFRWCLXSICSD-LKR-----SLGFVSKVEACDSDLVDTVFNVTWTLG--CRPFM 177  
DB 644 INFDDCASNPCHIGICMDGINRYSCVSPGFTG--QRCNIDIDECASNPCKRGATCINGV 701

QY 178 NSORAAICAE 188  
DB 702 NGFR--CICPE 710

## RESULT 14

US-08-532-384-19  
; Sequence 19, Application US/08532384  
; Patent No. 6083904  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, S. et al.  
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods  
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And  
; TITLE OF INVENTION: Nucleic Acids  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,384  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/083,590  
; FILING DATE: 25-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 8698864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2471 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-532-384-19

Query Match 7.3%; Score 77.5; DB 3; Length 2471;  
Best Local Similarity 23.6%; Pred. No. 19;  
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;

QY 63 VCOY-----RCRYGKAPMPRP-GYKQEPNGCGSYFLGLKVPESMDL-----103  
DB 528 VQCIDIDDCSSTPCINGAKCIDHPNGYEQ-----CATGFTGVLCEENIDNCDDPPCHHGQ 583

QY 104 ---GIPAMTKCCN-----QLDVCYDTGANKYRC-----129  
DB 584 CQGDIDSYTCINPGYMGALCSQDIDECYSSPCINDGRCDLVNGYQCNCQPGTGVNCE 643

QY 130 ----DAKFRWCLXSICSD-LKR-----SLGFVSKVEACDSDLVDTVFNVTWTLG--CRPFM 177

Db 644 INFDDCASNPCIHGICMDGINRYSCVSPGFTG--QRCNIDIDECASNPCRKGATCINGV 701  
Qy 178 NSQRAACICAE 188  
Db 702 NGRF--CICPE 710

RESULT 15  
US-08-899-232-1  
; Sequence 1, Application US/08899232  
; Patent No. 6436650  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Qi, Huilin  
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON  
; FILE REFERENCE: 7326-046  
; CURRENT APPLICATION NUMBER: US/08/899,232  
; CURRENT FILING DATE: 1997-07-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2471  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-899-232-1

Query Match 7.3%; Score 77.5; DB 4; Length 2471;  
Best Local Similarity 23.6%; Pred. No. 19;  
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;  
Qy 63 VCQY-----RCRYGKAPMPRP-GYKQEPNGCGSYFLGLKVPESMDL----- 103  
Db 528 VCQIDIDDSCSTPCLNGAKCIDHENGVEQ---CATGFTGVLCENIDNCDDPDCHHGQ 583  
Qy 104 ---GIPAMTKCCN-----QLDVCTCGANKYRC----- 129  
Db 584 CQDGIDSYTCICNPGYMGAIQDIDECYSSPCLNDGRCIDLNVGYQCNCQFGTSGVNCE 643  
Qy 130 -----DAKFRMCLXISCD-LKR-----SLGFVSKVEACDSLVDTVFNTVWTLG--CRPFM 177  
Db 644 INFDDCASNPCIHGICMDGINRYSCVSPGFTG--QRCNIDIDECASNPCRKGATCINGV 701  
Qy 178 NSQRAACICAE 188  
Db 702 NGRF--CICPE 710

Search completed: May 17, 2004, 10:48:07  
Job time : 23 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:43:49 ; Search time 46 Seconds  
(without alignments)

1173.537 Million cell updates/sec

Title: US-10-621-401-145

Perfect score: 1066

Sequence: 1 MKLASGFLVLSLGGGLAQ.....PFMSQRAACIAEBEKEEL 194

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1064	99.8	194	10	US-09-974-879-145
2	1064	99.8	194	12	US-10-621-401-145
3	1064	99.8	194	12	US-10-363-616-357
4	1064	99.8	195	10	US-09-305-736-144
5	1064	99.8	195	11	US-09-818-683-144
6	467	43.8	192	9	US-09-993-999-4
7	460.5	43.2	194	9	US-09-975-374A-13
8	459	43.1	182	9	US-09-975-374A-10
9	458	43.0	189	9	US-09-867-550-1504
10	458	43.0	189	9	US-09-993-999-2
11	458	43.0	189	9	US-09-975-374A-2
12	458	43.0	189	12	US-10-147-493-240
13	458	43.0	189	12	US-10-145-127-240
14	458	43.0	189	12	US-10-160-503-240
15	458	43.0	189	12	US-10-169-395-97

16	458	43.0	189	12	US-10-143-118-240
17	458	43.0	189	12	US-10-144-993-240
18	458	43.0	189	12	US-10-158-787-240
19	458	43.0	189	12	US-10-140-024-240
20	458	43.0	189	12	US-10-140-808-240
21	458	43.0	189	12	US-10-152-405-240
22	458	43.0	189	12	US-10-127-852A-240
23	458	43.0	189	12	US-10-128-685A-240
24	458	43.0	189	12	US-10-128-685A-240
25	458	43.0	189	12	US-10-131-820A-240
26	458	43.0	189	12	US-10-142-886-240
27	458	43.0	189	12	US-10-146-728-240
28	458	43.0	189	12	US-10-146-786-240
29	458	43.0	189	12	US-10-147-499-240
30	458	43.0	189	12	US-10-157-798-240
31	458	43.0	189	14	US-10-028-072-240
32	458	43.0	189	14	US-10-121-043-240
33	458	43.0	189	14	US-10-123-904-240
34	458	43.0	189	14	US-10-140-474-240
35	458	43.0	189	14	US-10-175-746-240
36	458	43.0	189	14	US-10-176-918-240
37	458	43.0	189	14	US-10-176-921-240
38	458	43.0	189	14	US-10-137-865-240
39	458	43.0	189	14	US-10-140-474-240
40	458	43.0	189	14	US-10-142-431-240
41	458	43.0	189	14	US-10-143-114-240
42	458	43.0	189	14	US-10-140-003-240
43	458	43.0	189	14	US-10-142-419-240
44	458	43.0	189	14	US-10-123-262-240
45	458	43.0	189	14	US-10-142-423-240

#### ALIGNMENTS

#### RESULT 1

US-09-974-879-145  
; Sequence 145, Application US/09974879  
; Publication No. US20030028003A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 125 Human Secreted Proteins  
; FILE REFERENCE: P2020P2  
; CURRENT APPLICATION NUMBER: US 09/974,879  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/239,893  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 09/818,683  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 09/305,736  
; PRIOR FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: PCT/US98/23435  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: US 60/064,911  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,912  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,983  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,900  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,988  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,987  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,908  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,984  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,985  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/066,094  
; PRIOR FILING DATE: 1997-11-17

```
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (138)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-974-879-145

Query Match          99.8%; Score 1064; DB 10; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-108;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRPGYKQEPNCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRPGYKQEPNCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120

QY 121 TCGANKYRCDKAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDKAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180

QY 181 RAAICAEKEEKEEL 194
DB 181 RAAICAEKEEKEEL 194

RESULT 2
US-10-621-401-145
; Sequence 145, Application US/10621401
; Publication No. US20040038277A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020F2C1
; CURRENT APPLICATION NUMBER: US/10/621,401
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/974,879
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 611
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (138)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-621-401-145

Query Match          99.8%; Score 1064; DB 12; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-108;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRPGYKQEPNCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRPGYKQEPNCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120

QY 121 TCGANKYRCDKAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDKAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180

QY 181 RAAICAEKEEKEEL 194
DB 181 RAAICAEKEEKEEL 194

RESULT 3
US-10-363-616-357
; Sequence 357, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 357
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-357

Query Match          99.8%; Score 1064; DB 12; Length 194;
Best Local Similarity 99.5%; Pred. No. 1.7e-108;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRPGYKQEPNCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRPGYKQEPNCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120

QY 121 TCGANKYRCDKAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDKAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180

QY 181 RAAICAEKEEKEEL 194
DB 181 RAAICAEKEEKEEL 194

RESULT 4
```

[illegible]



```
Db 65 YKSDGSKPFRYGYKSPNPGCGSPLFGV-----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFSVSKVEACDSLVDTVNTVTLGCRPFMNSORAAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVLLFSDVHLGCKPYLDSORAAACR 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 10
US-09-993-999-2
; Sequence 2, Application US/09993999
; Patent No. US20020110891A1
; GENERAL INFORMATION:
; APPLICANT: Ho, I-Cheng
; APPLICANT: Arm, Jonathan P.
; APPLICANT: Austen, K. Frank
; APPLICANT: Glimcher, Laurie H.
; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
; TITLE OF INVENTION: Expressed in Th2 Cells
; FILE REFERENCE: HUI-046
; CURRENT APPLICATION NUMBER: US/09/993,999
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,316
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-993-999-2

Query Match 43.0%; Score 458; DB 9; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHGRGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT-----TDMRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCRYGKAPMPRPGYKPOEPNPGCGSYFLGLKVPESMDLGIKAMTKCCNQLDVCDYDTCCAN 125
Db 65 YKSDGSKPFRYGYKSPNPGCGSPLFGV-----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFSVSKVEACDSLVDTVNTVTLGCRPFMNSORAAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVLLFSDVHLGCKPYLDSORAAACR 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 11
US-09-975-374A-2
; Sequence 2, Application US/09975374A
; Patent No. US20020119139A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: CLONING AND RECOMBINANT EXPRESSION OF MAMMALIAN GROUP
; TITLE OF INVENTION: X11 SECRETED PHOSPHOLIPASE A2
; FILE REFERENCE: 1479-R-00
; CURRENT APPLICATION NUMBER: US/09/975,374A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/239,489
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHGRGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT-----TDMRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCRYGKAPMPRPGYKPOEPNPGCGSYFLGLKVPESMDLGIKAMTKCCNQLDVCDYDTCCAN 125
Db 65 YKSDGSKPFRYGYKSPNPGCGSPLFGV-----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFSVSKVEACDSLVDTVNTVTLGCRPFMNSORAAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVLLFSDVHLGCKPYLDSORAAACR 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 12
US-10-147-493-240
; Sequence 240, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHGRGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT-----TDMRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCRYGKAPMPRPGYKPOEPNPGCGSYFLGLKVPESMDLGIKAMTKCCNQLDVCDYDTCCAN 125
Db 65 YKSDGSKPFRYGYKSPNPGCGSPLFGV-----HLNIGIPSLTKCCNQHDRCYETCGKS 120
```

```
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-374A-2

Query Match 43.0%; Score 458; DB 9; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHGRGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT-----TDMRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCRYGKAPMPRPGYKPOEPNPGCGSYFLGLKVPESMDLGIKAMTKCCNQLDVCDYDTCCAN 125
Db 65 YKSDGSKPFRYGYKSPNPGCGSPLFGV-----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFSVSKVEACDSLVDTVNTVTLGCRPFMNSORAAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVLLFSDVHLGCKPYLDSORAAACR 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 12
US-10-147-493-240
; Sequence 240, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHGRGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT-----TDMRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCRYGKAPMPRPGYKPOEPNPGCGSYFLGLKVPESMDLGIKAMTKCCNQLDVCDYDTCCAN 125
Db 65 YKSDGSKPFRYGYKSPNPGCGSPLFGV-----HLNIGIPSLTKCCNQHDRCYETCGKS 120
```

```
QY 126 KYRCDAKFRWCLXSTCSDLKRSIGFVSKVEACDSLVDTVNTVTLGCRPFMNSORAAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVLLEFDSVHLGCKPYLDSORAAACR 180
QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189

RESULT 13
US-10-145-127-240
; Sequence 240, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-145-127-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSGGGLAQSDTSPDTEESYSDW--GLRHLSGFESVNSYFDSFLELLGKNGVCQ 65
Db 9 LTLTLLMAAVRQEQAOQT----TDMRATLKIRNGVHKIDTYLNAALDILGGEDGLCQ 64
QY 66 YRCRYGKAPMRPGYKPOEPNGCGSYFLGLKVPESMDLIGIPAMTKCCNQLDVCYDTCCAN 125
Db 65 YKCSGSKPFPYRGYKPSPPNGCGSPFLGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKRSIGFVSKVEACDSLVDTVNTVTLGCRPFMNSORAAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVLLEFDSVHLGCKPYLDSORAAACR 180
QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189

RESULT 14
US-10-160-503-240
; Sequence 240, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C446
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-160-503-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSGGGLAQSDTSPDTEESYSDW--GLRHLSGFESVNSYFDSFLELLGKNGVCQ 65
Db 9 LTLTLLMAAVRQEQAOQT----TDMRATLKIRNGVHKIDTYLNAALDILGGEDGLCQ 64
QY 66 YRCRYGKAPMRPGYKPOEPNGCGSYFLGLKVPESMDLIGIPAMTKCCNQLDVCYDTCCAN 125
Db 65 YKCSGSKPFPYRGYKPSPPNGCGSPFLGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKRSIGFVSKVEACDSLVDTVNTVTLGCRPFMNSORAAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVLLEFDSVHLGCKPYLDSORAAACR 180
QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189

RESULT 15
US-10-169-395-97
; Sequence 97, Application US/10169395
; Publication No. US20040034192A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: KIMURA, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING
; FILE REFERENCE: 01997, 015100, US
; CURRENT APPLICATION NUMBER: US/10/169,395
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: JP 2000-585
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-588
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-2299
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-26862
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: JP 2000-58367
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/JP00/09359
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 150
```

```
; SEQ ID NO 97
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-395-97

Query Match      43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSDTSPTEESYSIW--GLRHLRGSPFVSNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLILLMAAVRQCQAQT---TDWRATLKTIRNGVHKIDTYLNAALDLLGGEDGLCQ 64

QY 66 YRCRYGKAPMPRPYKQBPNGCGSYFLGLKVPESMDLGIPIAMTKGCNOLDVCYDTCGAN 125
Db 65 YKCDGSKPFPYGYKPSPPNGCGSPLFGV---HLNIGIPSLTKCNQHDRCYETCGKS 120

QY 126 KYRCDAKFRWCLXISICSDLKRSIGFVSKVEACDSLVDTVFTNTVLGCRPFMNSORAAAI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETTVELLFDSEVHLGCKPYLDSQRAACK 180

QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189
```

Search completed: May 17, 2004, 10:49:38  
Job time : 47 secs

1	87	8.2	768	2	I53821	P-selectin - rat
2	86.5	8.1	819	2	T10355	hypothetical prote
3	84.5	7.9	389	2	I49263	potential oncogene
4	84.5	7.9	389	2	A59392	Wnt10b protein pre
5	84	7.9	798	2	S01659	integrin beta-1 ch
6	84	7.9	799	1	IUMSFB	fibronectin recept
7	83.5	7.8	573	2	S36028	urease (EC 3.5.1.5
8	81	7.6	2180	2	T29764	hypothetical prote
9	80.5	7.6	304	2	A33274	insulin-like growt
10	80.5	7.6	572	2	AC0325	urease (EC 3.5.1.5
11	80.5	7.6	1051	2	D83428	chitodextrinase VC
12	80	7.5	414	2	B96808	protein F28K19.2 [
13	80	7.5	799	2	JC4126	integrin beta olig
14	80	7.5	823	2	S18968	cyttestin precurs
15	80	7.5	3051	2	S42373	hypothetical prote
16	79.5	7.5	310	2	A60967	insulin-like growt
17	79	7.4	411	2	A65184	arylsulfatase acti
18	79	7.4	712	2	T16338	hypothetical prote
19	78.5	7.4	293	2	T31840	hypothetical prote
20	78.5	7.4	1820	2	A55494	latent transformin
21	78	7.3	601	2	B36346	fibulin 1 precursor
22	78	7.3	683	2	C36346	fibulin 1 precursor
23	78	7.3	710	2	I48668	zinc finger protei
24	77.5	7.3	153	2	T19054	hypothetical prote
25	77.5	7.3	187	2	G85343	phospholipase A2-1
26	77.5	7.3	1054	2	T30933	chitinase (EC 3.2.
27	77	7.2	353	2	I55572	maternal protein -
28	77	7.2	411	2	B91220	probable arylsulfa
29	77	7.2	411	2	D86066	probable arylsulfa



A:Molecule type: DNA

A:Residues: 1-819 <AHR>

A:Cross-references: EMBL:U75930; NID:g2934903; PID:g1911332

Query Match 8.1%; Score 86.5; DB 2; Length 819;

Best Local Similarity 24.7%; Pred. No. 3.9;

Matches 45; Conservative 22; Mismatches 62; Indels 53; Gaps 9;

Qy 46 VNSYF-----DSFLELLGGKGV--CQYRCYKAPMPREGYKQBPNGCGSYFLGLKV 97

Db 234 VLAYFPETLRVNEFVECKGKHVVARCPDQOVFORALMTCVQTHPCAFNGAGHTYI----- 289

Qy 98 PESWDLGPAMTKCNQLDVCYDTC-----CAN-KYRCDAKFRCLXISICDLKXSLG-- 149

Db 290 --TADIGDAQFFKCLNDREAOILITCNKRVGADGQYACSGDAR-----CADLPDGTGRL 341

Qy 150 -----FVSKVEACDS-----LVDFVNTVMTLGCPRFMNSQRAACI 185

Db 342 MHTHTDDTFEYVSGQTICDNYNIVISEIECDTGNVLNKL FVNKFTLGAQ-PPREVLDAGV 400

Qy 186 CA 187

Db 401 CA 402

RESULT 3

I49263

potential oncogene - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I49263

R:Lee, F.S.; Lane, T.F.; Kuo, A.; Shackelford, G.M.; Leder, P.

Proc. Natl. Acad. Sci. U.S.A. 92, 2268-2272, 1995

A:Title: Insertional mutagenesis identifies a member of the Wnt gene family as a candidate

A:Reference number: I49263; MUID:95199333; PMID:7892260

A:Accession: I49263

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-389 <RES>

A:Cross-references: EMBL:U20658; NID:g1020149; PIDN:AAA80110.1; PID:g677918

C:Genetics:

A:Superfamily: int-1 transforming protein

Query Match 7.9%; Score 84.5; DB 2; Length 389;

Best Local Similarity 22.0%; Pred. No. 3.1;

Matches 29; Conservative 15; Mismatches 41; Indels 47; Gaps 5;

Qy 59 GKNGVCQYRCRYKAPMPR-----LGIPAMT-KCCNQLDVCYDTCGA-----PGYKQBPNGCGSY 91

Db 251 GTSGCQFKTCWRAAPEFRAIGALRERLSRAIFIDITHNRNSGAFQPLRPRLRSLGELVY 310

Qy 92 FLGLKVPESMD-----LGIPAMT-KCCNQLDVCYDTCGA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTLGSPTGRACNKTSLRLDGGSLCCGGRGHNVLRQTRVERCHCRF 368

Qy 134 RWCLXISICDLK 145

Db 369 HWCCVYLCDECK 380

RESULT 4

A59392

Wnt10b protein precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001

C:Accession: A59393; A59392

R:Lee, F.S.; Lane, T.F.; Kuo, A.; Shackelford, G.M.; Leder, P.

Proc. Natl. Acad. Sci. U.S.A. 92, 2268-2272, 1995

A:Title: Insertional mutagenesis identifies a member of the Wnt gene family as a candidate

A:Reference number: A59393; MUID:95199333; PMID:7892260

A:Accession: A59393

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-389 <LEB>

A:Cross-references: GB:U20658; NID:g1020149; PID:g1351425; PIDN:AAA80110.1

Wang, J.; Shackelford, G.M.

Oncogene 13, 1537-1544, 1996

A:Title: Murine Wnt10a and Wnt10b: cloning and expression in developing limbs, face and

A:Reference number: A59392; MUID:96269404; PMID:8875992

A:Accession: A59392

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-389 <WAN>

A:Cross-references: GB:U61970; NID:g1546014; PID:g1546015; PIDN:AA08086.1

A:Note: proto-oncogene, potential transforming capacity, secreted protein, developmental

C:Superfamily: int-1 transforming protein

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-389/Product: Wnt10b protein #status predicted <MAR>

Query Match 7.9%; Score 84.5; DB 2; Length 389;

Best Local Similarity 22.0%; Pred. No. 3.1;

Matches 29; Conservative 15; Mismatches 41; Indels 47; Gaps 5;

Qy 59 GKNGVCQYRCRYKAPMPR-----PGYKQBPNGCGSY 91

Db 251 GTSGCQFKTCWRAAPEFRAIGALRERLSRAIFIDITHNRNSGAFQPLRPRLRSLGELVY 310

Qy 92 FLGLKVPESMD-----LGIPAMT-KCCNQLDVCYDTCGA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTLGSPTGRACNKTSLRLDGGSLCCGGRGHNVLRQTRVERCHCRF 368

Qy 134 RWCLXISICDLK 145

Db 369 HWCCVYLCDECK 380

RESULT 5

S01659

Integrin beta-1 chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 20-Aug-1999

C:Accession: S01659

R:Tominaga, S.I.

FEBS Lett. 238, 315-319, 1988

A:Title: Murine mRNA for the beta-subunit of integrin is increased in BALB/c-3T3 cells

A:Reference number: S01659; MUID:89005707; PMID:3262537

A:Accession: S01659

A:Molecule type: mRNA

A:Residues: 1-798 <TOM>

A:Cross-references: EMBL:Y00769; NID:g52721; PIDN:CAA68738.1; PID:g52722

A:Note: the authors translated the codon ATT for residue 696 as Leu

C:Superfamily: integrin beta chain; laminin-type EGF-like homology

C:Keywords: cell adhesion; cytoskeleton; duplication; heterodimer; membrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:71-798/Product: Integrin beta-1 chain #status predicted <MAT>

Query Match 7.9%; Score 84; DB 2; Length 798;

Best Local Similarity 26.8%; Pred. No. 6.5;

Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;

Qy 26 DTEESYSDWGLRHRLGSP-ESVNSYFDSFLELLGKNGVCQYRCRYKAPMPRPGYKQPE 84

Db 543 NTNEIYS-----GKPCEDNFCNDRSNGLICGGNGVC--RCRVCE----- 580

Qy 85 PNGCGSYFLGLKVPESMDLG--IPAMTKCCNQLDVCYDTCGANKYRC-DAKFRWCLXISIC 141

Db 581 ---CYPNTGSGACDCSLDTGPGCLASNGQICNGRGIC--ECGACK--CTDPFQF---GPTC 630

Qy 142 SDLKESLGFVSKVEACDSLVDTVFNTVTLGCRPFMNSQRAACICAE 189

Db 631 ETCQCTGLGVCAEHKEC-----VQCRAF-NKGKKKDTCAQE 664

RESULT 6

IJMSFB

fibronectin receptor beta chain precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-Jul-1999  
 C:Accession: P10104; B60587  
 R:Hollers, V.M.; Ruff, T.G.; Parks, D.L.; McDonald, J.A.; Ballard, L.L.; Brown, E.J.  
 J. Exp. Med. 169, 1589-1605, 1989  
 A>Title: Molecular cloning of a murine fibronectin receptor and its expression during in  
 for histocompatibility complex class II.  
 A:Reference number: P10103; MUID:89235580; PMID:2523953  
 A:Accession: P10104  
 A:Molecule type: mRNA  
 A:Residues: 1-799 <HOL>  
 A:Cross-references: GB:X15202; GB:Y00818; NID:G50986; PIDN:CAA33272.1; PID:G762977  
 A:Experimental source: strain BALB/c  
 A>Note: the cDNA clone was missing the first nucleotide of Met-1  
 R:Ryseck, R.P.; Macdonald-Bravo, H.; Zerlial, M.; Bravo, R.  
 Exp. Cell Res. 180, 537-545, 1989  
 A>Title: Coordinate induction of fibronectin, fibronectin receptor, tropomyosin, and act  
 A:Reference number: A60597; MUID:89121031; PMID:2521606  
 A:Accession: B60597  
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 596-799 <RYS>  
 C:Comment: The receptor is a heterodimer of alpha and beta chains.  
 C:Superfamily: integrin beta chain; laminin-type EGF-like homology  
 C:Keywords: Cell adhesion; duplication; glycoprotein; heterodimer; receptor; transmembra  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-799/Product: fibronectin receptor beta chain #status predicted <MAT>  
 F:21-729/Domain: extracellular #status predicted <EXT>  
 F:730-752/Domain: transmembrane #status predicted <TRA>  
 F:753-799/Domain: intracellular #status predicted <INT>  
 F:50,94,97,212,269,363,406,417,482,521,585,670/Binding site: carbohydrate (Asn) (covalen  
 Query Match 7.9%; Score 84; DB 1; Length 799;  
 Best Local Similarity 26.8%; Pred. No. 6.5;  
 Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;  
 QY 26 DTEESYSDWGLRHRLGSP--ESVNSYFDSLELLGGKNGVCQYRCRYGKAPMPRPYKPOE 84  
 DB 544 NTNEIYS-----GKFCEDNFNCDNRSLGICGGNGVC--RCRVCE----- 581  
 QY 85 PNGGSSYFLGLKVPESMDLG--IPAMTKCNQDVCYDTGCGANKYRC-DAKFRWCLXSTC 141  
 DB 582 ---CYPNYTGSCDCSLDTGPGCLASNGQICNGRGIC--PCGACK--CTDPKFKQ---GPTC 631  
 QY 142 SDLKRSGLGVSKVEACDLSLVDVTFVNTVTLGCRPFMNSQRAACICAE 189  
 DB 632 EFCQCLGLVCAEHKEC-----VQCRAP-NKGEKDTCAQE 665  
 RESULT 7  
 S36028  
 A:Alternate names: yuuc - Yersinia enterocolitica.  
 C:Species: Yersinia enterocolitica  
 C>Date: 03-Mar-1994 #sequence\_revision 03-Aug-1995 #text\_change 06-Jan-2003  
 C:Accession: S36028; S31419  
 R:Skurnik, M.  
 submitted to the EMBL Data Library, December 1992  
 A:Reference number: S36028  
 A:Accession: S36028  
 A:Molecule type: DNA  
 A:Residues: 1-573 <SKU>  
 A:Cross-references: EMBL:Z18865; NID:G1016360; PIDN:CAA79316.1; PID:G296319  
 R:Skurnik, M.; Bateford, S.; Mertz, A.; Schilz, E.; Toivanen, P.  
 submitted to the EMBL Data Library, December 1992  
 A:Description: The putative arithrogenic cationic 19 kD antigen of Yersinia enterocolib  
 A:Reference number: S31417  
 A:Accession: S31419  
 A:Molecule type: DNA  
 A:Residues: 1-59 <SK2>  
 A:Cross-references: EMBL:Z18865  
 C:Genetics:

A:Gene: yuuc  
 C:Superfamily: urease, alpha subunit; urease 62K chain homology  
 C:Keywords: hydrolase  
 F:4-556/Domain: urease 62K chain homology <U62>  
 Query Match 7.8%; Score 83.5; DB 2; Length 573;  
 Best Local Similarity 25.8%; Pred. No. 5.4;  
 Matches 31; Conservative 17; Mismatches 49; Indels 23; Gaps 5;  
 QY 15 GGGLAQSDTSPDTEESYSDWGLRHRLGSPES--VNSYFDSLELLGGKNGVCQYRCRYGK 72  
 DB 162 GGGIGFTDGTGTTTPGPNIRQLRSVEGLPVN-----VGILGKNS-----YGR 208  
 QY 73 APMPRP-----GYKQPPNGCGSYFL--GLKVPESMDLGIPAMTKCNQDVCYDTGCA 124  
 DB 209 GPLLEQATAGVVGKVKHEDWGATANALRHSLRMADEMDLIQSVHDSLNCEGYVEETIDA 268  
 RESULT 8  
 T29764  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Aug-2000  
 C:Accession: T29764  
 R:Du, Z.; Le, T.T.  
 submitted to the EMBL Data Library, May 1997  
 A:Description: The sequence of C. elegans cosmid T21E3.  
 A:Reference number: Z20681  
 A:Accession: T29764  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-2180 <DUZ>  
 A:Cross-references: EMBL:AF003133; PIDN:AA54138.1; GSPDB:GN00019; CESP:T21E3.3  
 A:Experimental source: strain Bristol N2; clone T21E3  
 C:Genetics:  
 A:Gene: CESP:T21E3.3  
 A:Map position: 1  
 A:Introns: 400/2; 1608/3; 1644/1; 1674/3; 1686/2; 1731/2; 2073/1; 2098/2; 2146/3  
 C:Superfamily: LDL receptor ligand-binding repeat homology  
 F:15-49/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
 F:51-85/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
 F:90-132/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
 F:149-185/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
 F:190-225/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
 F:229-272/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
 F:285-316/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
 F:323-359/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
 F:369-405/Domain: LDL receptor ligand-binding repeat homology <LDL9>  
 F:816-856/Domain: LDL receptor ligand-binding repeat homology <LDL10>  
 F:861-903/Domain: LDL receptor ligand-binding repeat homology <LDL11>  
 F:908-943/Domain: LDL receptor ligand-binding repeat homology <LDL12>  
 F:948-987/Domain: LDL receptor ligand-binding repeat homology <LDL13>  
 F:993-1027/Domain: LDL receptor ligand-binding repeat homology <LDL14>  
 F:1031-1063/Domain: LDL receptor ligand-binding repeat homology <LDL15>  
 F:1126-1165/Domain: LDL receptor ligand-binding repeat homology <LDL16>  
 F:1172-1209/Domain: LDL receptor ligand-binding repeat homology <LDL17>  
 F:1213-1246/Domain: LDL receptor ligand-binding repeat homology <LDL18>  
 Query Match 7.6%; Score 81; DB 2; Length 2180;  
 Best Local Similarity 24.8%; Pred. No. 31;  
 Matches 29; Conservative 16; Mismatches 30; Indels 42; Gaps 8;  
 QY 69 RYKAPMPRPYKPOEPNGCGSYFLGLKVPESMDLGIPAMTKCNQDVCYD-----T 121  
 DB 8 KFCSTRVCRPGY-----FNCNGN---GLCIPEQ-----KVCNRINDCANFADESNC 50  
 QY 122 CGANKYCDKAFRWCLXSTCISDLKRSGLGVSKVEACDLSLVDVTFVNTVTLGCRPFM 178  
 DB 51 CNNEFRQCS-----GACIPSKAR---CNHMQDCNDASDEI-----GC-PFRN 89  
 RESULT 9  
 A33274

insulin-like growth factor-binding protein 2 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1989 #sequence\_revision 22-Nov-1989 #text\_change 07-Jul-2003  
 C:Accession: A33274; A40149; A25016; C33570; A31355; A61119; C40403; A49170  
 R:Brown, A.L.; Chiarotti, L.; Orłowski, C.C.; Mehman, T.; Burgess, W.H.; Ackerman, E.J.  
 J. Biol. Chem. 264, 5148-5154, 1989  
 A>Title: Nucleotide sequence and expression of a cDNA clone encoding a fetal rat binding  
 A:Reference number: A33274; MUID:89174801; PMID:2538475  
 A:Accession: A33274  
 A:Molecule type: mRNA  
 A:Residues: 1-304 <BR>  
 A:CROSS-references: GB:J04486; NID:g203175; PIDN:AAA40829.1; PID:g203176  
 R:Margot, J.B.; Binkert, C.; Mary, J.L.; Landwehr, J.; Heinrich, G.; Schwander, J.  
 Mol. Endocrinol. 3, 1053-1060, 1989  
 A>Title: A low molecular weight insulin-like growth factor binding protein from rat: cDN  
 A:Reference number: A40149; MUID:90014825; PMID:2477691  
 A:Accession: A40149  
 A:Molecule type: protein  
 A:Residues: 1-297, 'A', 299-304 <MAR>  
 A:CROSS-references: GB:M31672; NID:g204734; PIDN:AAA41381.1; PID:g204735  
 R:Motola, C.; Macdonald, R.G.; Brackett, J.L.; Mole, J.E.; Anderson, J.K.; Czech, M.P.  
 J. Biol. Chem. 261, 11180-11188, 1986  
 A>Title: Purification and amino-terminal sequence of an insulin-like growth factor-bindi  
 A:Reference number: A25016; MUID:86278218; PMID:2426267  
 A:Accession: A25016  
 A:Molecule type: protein  
 A:Residues: 38-68 <NOT>  
 R:Shimonaka, M.; Schroeder, R.; Shimasaki, S.; Ling, N.  
 Biochem. Biophys. Res. Commun. 165, 189-195, 1989  
 A>Title: Identification of a novel binding protein for insulin-like growth factors in ad  
 A:Reference number: A33570; MUID:90073708; PMID:2480123  
 A:Accession: C33570  
 A:Molecule type: protein  
 A:Residues: 35-39, 'X', 41-42, 'X', 44-50, 'X', 52-58, 'X', 60-64 <SHI>  
 R:Wang, J.F.; Hampton, B.; Mehman, T.; Burgess, W.H.; Rechler, M.M.  
 Biochem. Biophys. Res. Commun. 157, 718-726, 1988  
 A>Title: Isolation of a biologically active fragment from the carboxy terminus of the fe  
 A:Reference number: A31355; MUID:89076308; PMID:2974285  
 A:Accession: A31355  
 A:Molecule type: protein  
 A:Residues: 178-204 <WAN>  
 R:Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, M.K.  
 Endocrinology 129, 1066-1074, 1991  
 A>Title: Developmental expression of rat insulin-like growth factor binding protein-2 by  
 A:Reference number: A61119; MUID:91309520; PMID:1713158  
 A:Accession: A61119  
 A:Molecule type: protein  
 A:Residues: 35-67 <OLS>  
 R:Shimasaki, S.; Shimonaka, M.; Zhang, H.P.; Ling, N.  
 J. Biol. Chem. 266, 10646-10653, 1991  
 A>Title: Identification of five different insulin-like growth factor binding proteins (I  
 A:Reference number: A40403; MUID:91244847; PMID:1709938  
 A:Accession: C40403  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 35-39, 'X', 41-42, 'X', 44-50, 'X', 52-57 <SH2>  
 R:Park, J.H.Y.; McCusker, R.H.; Vanderhoof, J.A.; Mohammadpour, H.; Harty, R.F.; MacDona  
 Endocrinology 131, 1359-1368, 1992  
 A>Title: Secretion of insulin-like growth factor II (IGF-II) and IGF-binding protein-2 b  
 A:Reference number: A49170; MUID:92371335; PMID:1380441  
 A:Accession: A49170  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 35-39, 'X', 41-42, 'X', 44-50, 'X', 52 <PAR>  
 C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat h  
 C:Keywords: plasma  
 F:1-34/Domain: signal sequence #status predicted <SIG>  
 F:35-304/Product: insulin-like growth factor binding protein 2 #status experimental <MAT  
 F:206-285/Domain: thyroglobulin type I repeat homology <THY1>  
 Query Match 7.6%; Score 80.5; DB 2; Length 304;  
 Best Local Similarity 22.8%; Pred. No. 5.7;  
 Matches 39; Conservative 25; Mismatches 60; Indels 49; Gaps 9;

Qy 26 DTBESYSDWGLRHRLGSEFVSNSYFDSFLELLGKNGVCQYRCRYGKAPMPGKYK---- 81  
 Db 129 DSEDDHSEGL-----VENHVDGTMNMLGGSSA-----GRKP-PKSGMKELAV 170  
 Qy 82 -----POEPNGCGSYFLGLKVPESMDLGPAMTKCCNOLDVCYDPCGANKYRCDAKFR 134  
 Db 171 FREKVNQHRQMGKGAHLSLEPKKL-RPPPARTPCQQLDQVLERISTWRLPDD---R 226  
 Qy 135 WCLXSICDLKRSIGFVSKVEACDLSLVDTVNTVWTL-GCRPFMNSORAAIC 186  
 Db 227 GPLFHLYS-----LHFPNCDK-----HGLYNLKQCKMSLNGRGECWC 264  
 RESULT 10  
 AC0325  
 urease (EC 3.5.1.5) alpha chain [imported] [imported] - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 06-Jan-2003  
 C:Accession: AC0325  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
 Nature 413, 523-527, 2001  
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AC0325  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-572 <KUR>  
 A:CROSS-references: GB:AL590842; PIDN:CAC92906.1; PID:g15980647; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: ureC  
 C:Superfamily: urease, alpha subunit; urease 62K chain homology  
 C:Keywords: hydrolase  
 Query Match 7.6%; Score 80.5; DB 2; Length 572;  
 Best Local Similarity 25.0%; Pred. No. 10;  
 Matches 30; Conservative 18; Mismatches 49; Indels 23; Gaps 5;  
 Qy 15 GGGAAQSDTSPDTBESYSDWGLRHRLGSEFVSNSYFDSFLELLGKNGVCQYRCRYGK 72  
 Db 161 GGGIGPTDGTGTGTTVTPGPMNIQRLRSIEGLPVN-----VGILGKNS-----YGR 207  
 Qy 73 APMREP-----GYKPPQPNCGSYFL--GLKVPESMDLGPAMTKCCNOLDVCYDTCGA 124  
 Db 208 GPLLEQAAGVGVYKVEDWGATATNAHLRAHMADEVDIQSVHTDSLNECGYVEDTIDA 267  
 RESULT 11  
 chitodextrinase VCA0700 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
 DB2428  
 C:Species: Vibrio cholerae  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C:Accession: DB2428  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, E.  
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: AB2035; MUID:20406833; PMID:10952301  
 A:Accession: DB2428  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1051 <HEI>  
 A:CROSS-references: GB:AE003853; NID:g9658111; PIDN:AAF96599.1; GSPDB:GN001  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VCA0700  
 A:Map position: 2  
 Query Match 7.6%; Score 80.5; DB 2; Length 1051;  
 Best Local Similarity 24.8%; Pred. No. 18;

Matches 27; Conservative 14; Mismatches 35; Indels 33; Gaps 4;  
QY 14 LGGLAQSDTSPPTESY-----SDWGLRLHSGSPES-----VNSYFD 51  
Db 569 VGHNAALYDTGKDSLAQNMVNYTAQYGGIGYLTNDWAXYFRGSPAGRINTGVPIYTR 628  
QY 52 SPLELLGGKNGVCQYRCRYKAMPR-----PGYKQPEPNCGSYFLGL 95  
Db 629 GWOGVTGGNGL-----WGRAALPNQNLCAPTGEGEKNGCHGATGI 671  
RESULT 12  
B96808  
protein F28K19.2 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: B96808  
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: B96808  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-414 <STO>  
A;Cross-references: GB:AE005173; NID:g6573782; PIDN:AAFL17702.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: F28K19.2  
A;Map position: 1  
Query Match 7.5%; Score 80; DB 2; Length 414;  
Best Local Similarity 29.1%; Pred. No. 8.5;  
Matches 32; Conservative 9; Mismatches 49; Indels 20; Gaps 6;  
QY 89 GSVFLGLKVPESMDLGLTPAMTKCNQDLVYDTCGANKYRCDAKFRCLXISCSDLKRL 148  
Db 298 GSWFLEGLVEHIDRNF-----CGTTPDCRWKAAGDV-CVASFWSGSGICKSVSR-- 349  
QY 149 GFYSKV--EACDSLVDTVNTVTLGCRPFMNSQRAACI-----CAEEK 191  
Db 350 ---WKIVHEVCSEGAWNTL--LQVPILNITLIDCYKKGKEREER 394  
RESULT 13  
JC4126  
integrin beta oligodendroglia chain precursor - rat  
N;Alternate names: integrin b1 chain precursor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 20-Aug-1999  
C;Accession: JC4126  
R;Malek-Hedayat, S.; Rome, L.H.  
Gene 158, 287-290, 1995  
A;Title: Cloning and sequence of the cDNA encoding the rat oligodendrocyte integrin beta  
A;Reference number: JC4126; MUID:95331632; PMID:7541764  
A;Accession: JC4126  
A;Molecule type: mRNA  
A;Residues: 1-799 <MAL>  
A;Cross-references: GB:U12309; NID:g520565; PIDN:AAA86669.1; PID:g520566  
C;Comment: This protein belongs to a superfamily of heterodimeric cell-surface glycoprob  
C;Superfamily: integrin beta chain; laminin-type EGF-like homology  
C;Keywords: glycoprotein; oligodendrocyte; transmembrane protein  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-799/Product: integrin beta oligodendroglia chain #status predicted <MAT>  
F;730-752/Domain: transmembrane #status predicted <TM>  
F;750,94,97,212,269,363,406,417,482,521,585,670/Binding site: carbohydrate (Asn) (covalen

Query Match 7.5%; Score 80; DB 2; Length 799;  
Best Local Similarity 26.6%; Pred. No. 15;  
Matches 45; Conservative 16; Mismatches 56; Indels 52; Gaps 12;  
QY 26 DTEESYSDNGLRHLRSP-ESVNSYFDSFLELLGGKNGVCQYRCRYKAMPRPGYKQPE 84  
Db 544 NTNEIYS-----GKFCEDCNFCDNRNGLTCGGNGVC--RCRVCE----- 581  
QY 85 PNGCGSYFLGLKVPESMDLGLIPAMT---KCCNQDLVYDTCGANKYRC-DAKFRWCLXSI 140  
Db 582 ---CYPNTYTGACDCSLDT-VPCVAINGQICNGRGIC--ECGACK--CTDPKQK---GPT 630  
QY 141 CSDLKRSLSGFVSKVEACDSLVDTVNTVTLGCRPFMNSQRAACICAE 189  
Db 631 CFCQTCLGVCAEHKEC-----VQCRAF-NKGEKKDTCQAE 665  
RESULT 14  
S18968  
cyttestin precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: I48784; S18968  
R;Senftleben, A.; Wallat, S.; Lemaire, L.; Heinlein, U.A.O.  
Dev. Growth Differ. 36, 49-58, 1994  
A;Title: Pre and postmeiotic germ cell specific expression of TAZ83, a gene encoding a f  
A;Reference number: I48784  
A;Accession: I48784  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-823 <RES>  
A;Cross-references: EMBL:X64227; NID:g54264; PID:g54265  
C;Genetics:  
A;Gene: TAZ83  
C;Superfamily: mouse meltrin alpha; disintegrin homology  
F;395-480/Domain: disintegrin homology <DIS>  
Query Match 7.5%; Score 80; DB 2; Length 823;  
Best Local Similarity 26.3%; Pred. No. 16;  
Matches 35; Conservative 16; Mismatches 44; Indels 38; Gaps 10;  
QY 81 KPDPNGCGSYFLGLKVPESMDLGLIP---AMTKCNQDL---VCYDTCGANKYRCDAKFR 134  
Db 392 QPQGGSYCGNHL--LEVPEQDCGPEPTCTHKCCNPKDCTLDAACGCTGPC-CDK--R 446  
QY 135 WCLXS---ICSDLKRSLSGFVSKVEACDSLVDTVNTVTLGCRPF-----MNSORA 182  
Db 447 TCTIAERGLCRKSKQDCF---PEFCNG-----ETEGCAPDTKAADLEPCNNETA 494  
QY 183 AC---ICAEKEE 192  
Db 495 YCFGVCRDPDRQ 507  
RESULT 15  
S42373  
hypothetical protein T20G5.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 07-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999  
C;Accession: S42373  
R;Smith, A.  
submitted to the EMBL Data Library, March 1994  
A;Reference number: S42368  
A;Accession: S42373  
A;Molecule type: DNA  
A;Residues: 1-3051 <SMI>  
A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485  
C;Genetics:  
A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;  
C;Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin t  
F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1>  
F;754-793/Domain: fibronectin type II repeat homology <2FI>  
F;1201-1244/Domain: EGF homology <EGF>

Query Match 7.5%; Score 80; DB 2; Length 3051;  
Best Local Similarity 24.0%; Pred. No. 52; Mismatches 57; Indels 64; Gaps 9;  
Matches 43; Conservative 15; Mismatches 57; Indels 64; Gaps 9;  
QY 42 SPESVNSYFDSFELELGGKNGVCQYRCRYGKAPMPRPGYKQPEP-----NGCGS 90  
Db 1960 SLNSCSAFADCFDE---ENG---YRCRC-----RNGYHDDDDPAHPGHRCSFMINCEDS 2006  
QY 91 YFGLKVPEMDLGIPTAMTKCCNQLDVCYDTGANKYRCDAKF-----RWCLXSI 140  
Db 2007 SNL-----NDCDRNANCIDTAGGYDCACKAFYRDEGPPQSPGRCRLNE 2050  
QY 141 CSDLKRSGLGVSKVEACDSLVD-TVFNVTWTLGCR-----PFMNSORAAACIAEBEKEE 193  
Db 2051 CLNPNRN-----TCDRNACRDLGYTCTCRHGFDQSPNPOEPGRICIEFQEE 2101

Search completed: May 17, 2004, 10:44:17  
Job time : 22 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:36:28 ; Search time 17 seconds  
(without alignments)  
594.212 Million cell updates/sec

Title: US-10-621-401-145

Perfect score: 1066

Sequence: 1 MKLAGFLVWLGLGGLAQ.....PFMNSQRAACICAEKEEKL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1053.5	98.8	195	1 PA2Z HUMAN	Q9bx93 homo sapien
2	946.5	88.8	195	1 PA2Z MOUSE	Q99p27 mus musculus
3	467	43.8	192	1 PA2Y MOUSE	Q9ep22 mus musculus
4	458	43.0	189	1 PA2Y HUMAN	Q9bzm1 homo sapien
5	88	8.3	396	1 POOE RAHAQ	Q33506 rahnella aq
6	87	8.2	768	1 LEM3 RAT	P98106 rattus norv
7	86.5	8.1	443	1 FBL4 CRIGR	O55058 cricetus
8	86.5	8.1	819	1 Y083 NVOP	O10336 orgyia pseu
9	84.5	7.9	389	1 WN1B MOUSE	P48614 mus musculus
10	84	7.9	798	1 ITB1 MOUSE	P09055 mus musculus
11	83.5	7.8	443	1 FBL4 HUMAN	O95967 homo sapien
12	83.5	7.8	571	1 UREL YEREN	P31494 versinia en
13	82.5	7.7	389	1 WN1B HUMAN	O00744 homo sapien
14	81.5	7.6	571	1 UREL YERPS	P52313 versinia ps
15	80.5	7.6	304	1 IBP2 RAT	P12843 rattus norv
16	80.5	7.6	431	1 NOCT HUMAN	Q9uk39 homo sapien
17	80.5	7.6	443	1 FBL4 MOUSE	O9wtj9 mus musculus
18	80.5	7.6	571	1 UREL YERPE	O9zif9 versinia pe
19	80	7.5	799	1 ITB1 RAT	P49134 rattus norv
20	80	7.5	3787	1 MUA3 CAEL	P34576 caenorhabdi
21	79.5	7.5	429	1 NOCT MOUSE	O35710 mus musculus
22	79	7.4	411	1 ASLB ECOLI	P25550 escherichia
23	78	7.3	703	1 FBL1 HUMAN	P23142 homo sapien
24	77.5	7.3	2471	1 NTC2 HUMAN	O04721 homo sapien
25	77	7.2	353	1 WN11 XENLA	P49893 xenopus lae
26	77	7.2	768	1 LEM3 MOUSE	Q01102 mus musculus
27	77	7.2	773	1 ITB1 BOVIN	P53712 bos taurus
28	77	7.2	798	1 ITB1 FELCA	P53713 felis silve
29	76.5	7.2	2470	1 NTC2 MOUSE	O35516 mus musculus
30	76	7.1	1195	1 KDGD HUMAN	O16760 homo sapien
31	75.5	7.1	142	1 PA22 HELSU	P80003 heloderma s
32	75.5	7.1	835	1 CD97 HUMAN	P48960 homo sapien
33	75.5	7.1	1025	1 CA16 MOUSE	Q04857 mus musculus

34	75	7.0	130	1 TAT SIWM1	P05911 simian immu
35	75	7.0	144	1 PA2A HUMAN	P14555 homo sapien
36	74.5	7.0	145	1 PA2M CAVPO	P47711 cavia porce
37	74.5	7.0	317	1 IBF2 SHEEP	Q29400 ovis aries
38	74.5	7.0	371	1 WNT1 XENLA	P10108 xenopus lae
39	74.5	7.0	509	1 PA23 HUMAN	Q9nz20 homo sapien
40	74.5	7.0	577	1 TRBM MOUSE	P15306 mus musculus
41	73.5	6.9	253	1 NOCT RAT	Q9et55 rattus norv
42	73.5	6.9	305	1 IBP2 MOUSE	P47877 mus musculus
43	73.5	6.9	328	1 IBF2 HUMAN	P18065 homo sapien
44	73.5	6.9	417	1 WN1A HUMAN	Q9gz75 homo sapien
45	73.5	6.9	777	1 UNCG CAEL	Q21774 caenorhabdi

ALIGNMENTS

RESULT 1  
PA2Z HUMAN  
ID PA2Z HUMAN STANDARD; PRT; 195 AA.  
AC Q9BX53; Q95Q99;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Group XIII secretory phospholipase A2-like protein precursor (GXIII  
DE sPLA2-like).  
GN PLA2G13 OR FKSG71.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takahashi K.;  
RT "Cloning of human group XIII secreted phospholipase A2.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Wang Y.-G., Gong L.;  
RT "Cloning and characterization of FKSG71, a novel gene encoding group  
RT XIII secreted phospholipase A2.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Not known; does not seem to have catalytic activity.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; AF349540; AA030168.1; --  
EMBL; AF339053; AAL09472.1; --  
Genew; HGNC:18555; PLA2G13  
InterPro; IPR000886; ER\_target\_S.  
InterPro; IPR001211; PhospholipaseA2.  
PROSITE; PS00119; PA2 ASP; FALSE NEG.  
PROSITE; PS00118; PA2 HIS; FALSE NEG.  
PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
Calcium; Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 195 GROUP XIII SECRETORY PHOSPHOLIPASE A2-  
FT LIKE PROTEIN.  
FT METAL 89 89 CALCIUM (VIA CARBONYL OXYGEN)  
FT (BY SIMILARITY).  
FT METAL 91 91 CALCIUM (VIA CARBONYL OXYGEN)  
FT (BY SIMILARITY).  
FT METAL 93 93 CALCIUM (VIA CARBONYL OXYGEN)  
FT (BY SIMILARITY).

FT	METAL	93	93	(BY SIMILARITY).
FT				CALCIUM (VIA CARBONYL OXYGEN)
FT				(BY SIMILARITY).
FT	METAL	116	116	CALCIUM (BY SIMILARITY).
FT	SEQUENCE	195 AA;	21736 MW;	86P8E653BD08DA2A CRC64;
QY	Query Match	88.8%;	Score 946.5;	DB 1; Length 195;
B	Best Local Similarity	88.7%;	Pred. No. 2.5e-85;	
M	Matches 173;	Conservative	4;	Mismatches 17; Indels 1; Gaps 1;
Dy				
QY	1	MKLASGFLVLWLSLGGLAQSDTSPDTEBSYSYDWGLRHRLRGSPESVNSYFDSFLELLGGK	60	
Dy	1	MKLKGFFLLMLGLVGNLAQSDSPKEEBSYSYDWGLRQLRGSPESVNSYVDSEWELLGGK	60	
QY	61	NGVCQRRCRYGKAPMPRPQYKQPENPGCGSYFLGLKVPSMDLIGIPAMTKCNCNOLDVCYD	120	
Dy	61	NGVCQRRCRYGKAPMPRPQYKQAQPNPGCSYFLGIKVPGSMDLIGIPAMTKCCNQLDV CYD	120	
QY	121	TGCANKYRCDAKFRWCXCLXSICDLKHSIGFSVKVE-ACDSLVDVTNTVTWLTCGRPFMNS	179	
Dy	121	TGCANKYRCDAKFRWCXCHSICDLKRTLFVSVEAACUSLADTVNTWTLCGRPFMNS	180	
QY	180	QRAACITCAEEKEEL	194	
Dy	181	QRAACITCAEEKEEL	195	
RESULT 3				
FAST MOUSE				
ID	FASY MOUSE	STANDARD;	PRT;	192 AA.
AC	Q9EPB2; Q9CQR3; Q9CTU1; Q9D7L3; Q9EPRI;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Group XII secretory phospholipase A2 precursor (EC 3.1.1.4)			
DE	[Phosphatidylcholine 2-acetylholase GXII] (GXII SPLA2).			
GN	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10030;			
[1]				
RN	SEQUENCE FROM N.A.			
RC	STRAIN=AKR;			
RC	MEDLINE=21264628; PubMed=11278438;			
HO	I.C., Arm J.P., Bingham C.O. III, Choi A., Austen K.F.,			
RA	Glimcher L.H.;			
RA	"A novel group of phospholipase A2s preferentially expressed in type			
RT	2 helper T cells."			
JL	J. Biol. Chem. 276:18321-18326(2001).			
[2]				
RN	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Embryo, and Tongue;			
RC	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyoawa H., Kondo S., Yamada I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustinchin S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lions P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Yawnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,			
RA	Hayaishizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection."			



```

RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TRISSUE=Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulcy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-en-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9SPR2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9SPR2-2; Sequence=VSP_004509;
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AY007381; AAC23336.1; -.
DR DR EMBL: AY007382; AAC23337.1; -.
DR EMBL: AK003183; -, NOT_ANNOTATED_CDS.
DR EMBL: AK009133; BAB26094.1; -.
DR EMBL: AK010011; BAB26641.1; -.
DR EMBL: AK010174; BAB26747.1; -.
DR EMBL: BC051117; AAH51117.1; -.
DR MGD: MGI:1913600; Pla2g12.
DR InterPro: IPR001211; PhospholipaseA2.
DR PROSITE: PS00119; PA2_ASP; FALSE_NEG.
DR PROSITE: PS00119; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Calcium; Signal; Alternative splicing.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 192
FT FT GROUP XII SECRETORY PHOSPHOLIPASE A2.
FT ACT_SITE 113 113 BY SIMILARITY.
FT ACT_SITE 128 128 BY SIMILARITY.
FT METAL 91 91 CALCIUM (VIA CARBONYL OXYGEN)
FT (BY SIMILARITY).
FT METAL 93 93 CALCIUM (VIA CARBONYL OXYGEN)
FT (BY SIMILARITY).
FT METAL 95 95 CALCIUM (VIA CARBONYL OXYGEN)
FT (BY SIMILARITY).
FT METAL 114 114 CALCIUM (BY SIMILARITY).
FT VARSPIC 1 73
FT FT MVTFPPAPSPALLLLLLATARGAQEQDQTDDTRATLKTI
FT FT NGKHIDYITNAALDLGGEDGLCQKSDG -> MKDYH
FT FT SGKGKEPFPFPGVGSGTEERGLRIGR (in isoform

```

[illegible]



AC	O33506;	
AD	10-OCT-2003 (Rel. 42, Created)	
AE	10-OCT-2003 (Rel. 42, Last sequence update)	
AF	10-OCT-2003 (Rel. 42, Last annotation update)	
AG	Coenzyme PQQ synthetase protein E (Pyrroloquinoline quinone biosynthesis protein E).	
AH	PQQE.	
AI	Rahnella aquatilis.	
AJ	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
AK	Enterobacteriaceae; Rahnella.	
AL	NCBI_TaxID=34038;	
AM	[1]	
AN	SEQUENCE FROM N.A.	
AO	STRAIN=ISL19;	
AP	MEDLINE=98146550; PubMed=9485602;	
AQ	Kim K.Y., Jordan D., Krishnan H.B.;	
AR	"Expression of genes from Rahnella aquatilis that are necessary for	
AS	mineral phosphate solubilization in Escherichia coli.";	
AT	FEMS Microbiol. Lett. 159:121-127(1998).	
AV	RL	
AW	- - COFACTOR: Iron-sulfur cluster (Potential).	
AX	- - PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.	
AY	- - SIMILARITY: Belongs to the radical SAM superfamily. PqqE family.	
AZ	-----	
BA	This SWISS-PROT entry is copyright. It is produced through a collaboration	
BB	between the Swiss Institute of Bioinformatics and the EMBL outstation	
BC	at the European Bioinformatics Institute. There are no restrictions on its	
BD	use by non-profit institutions as long as its content is in no way	
BE	modified and this statement is not removed. Usage by and for commercial	
BF	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
BG	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
BH	-----	
BI	EMBL; AF007584; AAC38153.1; -.	
BJ	HMAP; MF 00660; -; 1.	
BK	InterPro: IPR006638; ELP3.	
BL	InterPro: IPR000385; MoaA_NiFB_PqqE.	
BM	InterPro: IPR007197; Radical_SAM.	
BN	Pfam; PF04055; Radical_SAM; 1.	
BO	SMART; SM00729; ELP3; 1.	
BP	DR PROSITE; PS01305; MOA_NIFB_PQQE; FALSE_NEG.	
BQ	PQQ biosynthesis; Iron-sulfur.	
BR	METAL 41 41 IRON-SULFUR (POTENTIAL).	
BS	METAL 45 45 IRON-SULFUR (POTENTIAL).	
BT	METAL 48 48 IRON-SULFUR (POTENTIAL).	
BV	SEQUENCE 396 AA; 44381 MW; 26F16336445FDC00 CRC64;	
BW	-----	
BX	Query Match 8.3%; Score 88; DB 1; Length 396;	
BY	Best Local Similarity 27.0%; Pred. No. 0.4;	
BZ	Matches 37; Conservative 16; Mismatches 30; Indels 54; Gaps 11;	
CA	-----	
CB	QY 78 PGYKPEPNGC---GSYFLGLKVPESMDL-----GIPAMTKCNQL-DVCYDTC 132	
CC	254 PDYIERPRKCGMGWGAIFLSV-TPEGMALPCHSRQLPVEFPFSVLE--NTLQEIWYDSF 310	
CD	123 GANKYPCDAKFRW---CLKXSCISDLKRSIGFSVKVEACDSLVDVTWNTWTLGCR--PF 176	
CE	311 GFNKYR---GFDWMPEPCRS--CSEKEKDFG-----GCRQAF 343	
CF	177 M---NSQRAACTCAEE 190	
CG	344 MLTGNADNADPVCCKSE 360	
CH	-----	
CI	RESULT 6	
CJ	LEM3_RAT	
CK	ID LEM3_RAT STANDARD; PRT; 768 AA.	
CL	AC P98106;	
CM	DT 01-FEB-1996 (Rel. 33, Created)	
CN	DT 01-FEB-1996 (Rel. 33, Last sequence update)	
CO	DT 10-OCT-2003 (Rel. 42, Last annotation update)	
CP	DE P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)	
CQ	DE (CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (UECAM3).	
CR	OS SELP.	
CS	OS Rattus norvegicus (Rat).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=101116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=lung;  
 RX MEDLINE=94333817; PubMed=7520013;  
 RA Auchampach J.A., Oliver M.G., Anderson D.C., Manning A.M.;  
 RT "Cloning, sequence comparison and in vivo expression of the gene  
 encoding rat P-selectin.";  
 RL Gene 145:251-255(1994).  
 CC -|- FUNCTION: Ca(2+)-dependent receptor for myeloid cells that binds  
 CC to carbohydrates on neutrophils and monocytes. Mediates the  
 CC interaction of activated endothelial cells or platelets with  
 CC leukocytes. The ligand recognized is sialyl-Lewis X.  
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -|- TISSUE SPECIFICITY: Expressed in all tissues examined: spleen,  
 CC lung, brain, liver, heart, kidney, thymus and small intestine.  
 CC -|- INDUCTION: By acute inflammation (probable).  
 CC -|- SIMILARITY: Belongs to the selectin/LECAM family.  
 CC -|- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC -|- SIMILARITY: Contains 1 EGF-like domain.  
 CC -|- SIMILARITY: Contains 8 Sushi (SCR) domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L23088; AAA60325.1; -;  
 CC PIR; I53821; I53821.  
 CC HSP; P16109; IFSB.  
 CC InterPro; IPR006209; EGF like.  
 CC InterPro; IPR001304; Lectin\_C.  
 CC InterPro; IPR002396; Selectin.  
 CC InterPro; IPR000436; Sushi\_SCR\_CCP.  
 CC Pfam; PF00059; lectin\_c; 1.  
 CC Pfam; PF00084; sushi; 8.  
 CC PRINTS; PR00343; SELECTIN.  
 CC SMART; SM00032; CCR; 8.  
 CC SMART; SM00034; CLECT; 1.  
 CC PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 CC PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 1.  
 CC PROSITE; PS50026; EGF\_3; 1.  
 CC Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;  
 KW Selectin; Signal; Sushi; Repeat; Lipoprotein; Palmitate.  
 FT SIGNAL 1 41  
 FT CHAIN 42 768  
 FT DOMAIN 42 709  
 FT TRANSMEM 710 733  
 FT DOMAIN 734 768  
 FT DOMAIN 158 183  
 FT DOMAIN 159 195  
 FT DOMAIN 199 258  
 FT DOMAIN 261 320  
 FT DOMAIN 323 382  
 FT DOMAIN 385 444  
 FT DOMAIN 447 506  
 FT DOMAIN 509 568  
 FT DOMAIN 579 638  
 FT DOMAIN 641 700  
 FT DISULFID 60 158  
 FT DISULFID 131 150  
 FT DISULFID 168 183  
 FT DISULFID 185 194  
 FT DISULFID 200 244  
 FT DISULFID 230 257  
 FT DISULFID 262 306

FT DISULFID 292 319 BY SIMILARITY.  
 FT DISULFID 324 368 BY SIMILARITY.  
 FT DISULFID 354 381 BY SIMILARITY.  
 FT DISULFID 386 430 BY SIMILARITY.  
 FT DISULFID 416 443 BY SIMILARITY.  
 FT DISULFID 448 492 BY SIMILARITY.  
 FT DISULFID 478 505 BY SIMILARITY.  
 FT DISULFID 510 554 BY SIMILARITY.  
 FT DISULFID 540 567 BY SIMILARITY.  
 FT DISULFID 580 624 BY SIMILARITY.  
 FT DISULFID 610 637 BY SIMILARITY.  
 FT DISULFID 642 686 BY SIMILARITY.  
 FT DISULFID 672 699 BY SIMILARITY.  
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 654 654 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 661 661 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 679 679 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT LIPID 745 745 S-palmitoyl cysteine (By similarity).  
 FT SITE 756 759 ENDOCYTOSIS SIGNAL (PROBABLE).  
 SQ SEQUENCE 768 AA; 83517 MW; 26FD78A5F31316 CRC64;  
 Query Match 8.2%; Score 87; DB 1; Length 768;  
 Best Local Similarity 26.4%; Pred. No. 1.1;  
 Matches 37; Conservative 9; Mismatches 42; Indels 52; Gaps 8;  
 QY 38 HLKGSFE-----SYNSYFDSFLLELGGKNGVCQYRCYKAPMRPGYKPOEPNGCGS 90  
 Db 525 VHGGEFSVGSTCHFSCEE-----ELGSRNVECTVSGWSAPPTCKG----- 569  
 QY 91 YFLGLKVPESMDLGIPTAMT-----KCNQLD-----VCYDTC-----GANKYRCD 130  
 Db 570 -VTSLEVP---SVRCPALTPGQGTMSCHRHLESFGNTTCYFGCKTGTFTLGANSLRG 625  
 QY 131 AKFRW-----CLXSIKCSLD 144  
 Db 626 ASQWTAVTPVCAVKCSEL 645  
 RESULT 7  
 ID\_FBL4\_CRIGR STANDARD; PRT; 443 AA.  
 AC 055058;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE EGF-Containing fibulin-like extracellular matrix protein 2 precursor  
 DE (Fibulin-4) (FBLN-4) (H411 protein).  
 DE EFEMP2 OR FBLN4.  
 GN Cricetus griseus (Chinese hamster).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
 OX NCBI\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA Heine H., Delude R.L., Monks B., Golenbock D.T.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: Belongs to the fibulin family.  
 CC -|- SIMILARITY: Contains 6 EGF-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```

CC -----
CC EMBL; AF046870; AAC03101.1; -.
CC HSSP; P00736; 1A00.
CC InterPro; IPR000152; Asx_hydroxyl_s.
CC InterPro; IPR001861; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR001491; Thrbomodulin.
CC Pfam; PF00008; EGF; 4.
CC PRINTS; P00907; THRBOMODULN.
CC SMART; SM00179; EGF_CA; 4.
CC PROSITE; PS00010; ASX_HYDROXYL; 4.
CC PROSITE; PS00022; EGF_2; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 4.
CC PROSITE; PS00026; EGF_3; 4.
CC PROSITE; PS01187; EGF_CA; 6.
CC Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
KW SIGNAL 1 25
FT CHAIN 26 443
FT DOMAIN 36 81
FT EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT MATRIX PROTEIN 2.
FT EGF-LIKE 1, DIVERGENT.
FT EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT BY SIMILARITY.
FT DISULFID 127 140
FT DISULFID 134 149
FT DISULFID 151 162
FT DISULFID 168 177
FT DISULFID 173 186
FT DISULFID 188 201
FT DISULFID 207 217
FT DISULFID 213 226
FT DISULFID 228 241
FT DISULFID 247 258
FT DISULFID 254 267
FT DISULFID 269 281
FT DISULFID 287 300
FT DISULFID 294 309
FT DISULFID 315 327
FT CARBOHYD 198 198
FT CARBOHYD 394 394
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 443 AA; 49432 MW; 0BCE5D732D9E5F CRC64;

Query Match 8.1%; Score 86.5; DB 1; Length 443;
Best Local Similarity 22.2%; Pred. No. 0.64;
Matches 54; Conservative 19; Mismatches 71; Indels 99; Gaps 16;

QY 6 GFIVLV-----LSLGGGLAQSDDTSPDTEESYSD---WGL--RHLR-----GSF 43
DB 10 GSULLWALLLLGASPDSEPDSTECTDGYEWDADSQHCRDWNELTIPAEACKGEM 69
QY 44 ESNVSYFDSFLELLGGKNGVCQYRC-----RYGKAMP-----RFGYKP 82
DB 70 KCIHHY-----GG-----YLCLPSAAVINDLHGEGPPPPVPAQHPNCPGYPEP 115
QY 83 QEPNGGSGYFLGLKVPESMDLGIPTMYKC-----CNQLDVCYDTCGANKYR-----C--- 129
DB 116 DEQESC-----VDVDECAQALHDCRFSDCHNLPGSYQCTCPDGYRKVGPECVDI 165
QY 130 -DAKFRWCLXISCDLKRSL-----GF-----VSKVEACD-----SLVDVTFTVNTWL 171
DB 166 DECRYRYCQHR-CVNLPFSFRCQCEPQGLQPNRSCVDVNECDMGAPCQRCSNGTGF 224
QY 172 GCR 174
DB 225 LCR 227

RESULT 8
Y083_NPVOP

```

```

ID Y083_NPVOP STANDARD; PRT; 819 AA.
AC O10336;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical 91.1 kDa protein (ORF86).
OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpMNVPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OC NCBI_TaxID=164623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97271300; PubMed=9126251;
RA Ahrens C.H.; Russell R.R.; Funk C.J.; Evans J.; Harwood S.;
RA Rohmann G.F.;
RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
polyhedrosis virus genome."
RL Virology 229:381-399(1997).
CC -!- SIMILARITY: Contains 2 chitin-binding type-2 domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).


EMBL; U75930; AAC59085.1; -.
InterPro; IPR002557; Chitin_bind_PerA.
Pfam; PF01607; CBM 14; 1.
SMART; SM00494; ChEBD2; 1.
PROSITE; PS50940; CHIT_BIND_II; 2.
Hypothetical protein; Chitin-binding; Repeat.
FT SIGNAL 1 25
FT CHAIN 26 819
FT DOMAIN 150 230
FT DOMAIN 223 281
FT CHITIN-BINDING TYPE-2 1.
FT CHITIN-BINDING TYPE-2 2.
FT SEQUENCE 819 AA; 91067 MW; 108942AF0A8F925A CRC64;

Query Match 8.1%; Score 86.5; DB 1; Length 819;
Best Local Similarity 24.7%; Pred. No. 1.3;
Matches 45; Conservative 22; Mismatches 62; Indels 53; Gaps 9;

QY 46 VNSYF-----DSELELLGGKNGV--CQYRCYRGKAMP--PGYKQEPNGCGSYFLGLKV 97
DB 234 VIAYFPETURVNEFVECRGKGVVARCPDQVFDRLMTVCVTHPCAFNGAGHTYI--- 289
QY 98 PESMDLIGIPAMTKCCNQLDVCYDTC-----GAN-KYRCDAKFRWCLXISCDLKRSLG-- 149
DB 290 --TADIGDAQFFKCLNDREAQLITCINRVGADGGVACSGDAR-----CADLPDGTGRL 341
QY 150 -----FVSKVEACDS-----LVDTFTVNTVWTLGCPFPNPSQBAACI 185
DB 342 MHTHTDDTFEYVSGQTICDNYNVISEICTGNVLENKLFVNKFTLGAQ-FPREVLDAVG 400
QY 186 CA 187
DB 401 CA 402

RESULT 9
WN1B_MOUSE
ID WN1B_MOUSE STANDARD; PRT; 389 AA.
AC P48614; P70702;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Wnt-10b protein precursor (Wnt-12).
GN WNT10B OR WNT-10B OR WNT10 OR WNT12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.


```

Query Match	7.9%;	Score 84.5;	DB 1;	Length 389;
Best Local Similarity	22.0%;	Pred. No. 0.86;		
Matches	29;	Conservative 15;	Mismatches 41;	Indels 47; Gaps 5;

  

QY	59	GKNGVCQYCRYGKAMPR-----	-----PGYKQPDPNGCGSY 91
Db	251	GTSGSQFQKTCWRAAPEFAIGAALRELRISRAIFDTHNRNSGAFQRLRPRRLSGELVY 310	
QY	92	FLGLKVPESMD---LGIAPMT-KCCNOLDVCVDTGCA-----	-----NKYRCDAKF 133
Db	311	F--EKSPDFCERDPTLGSPTGRACNKTSRLDGGSLCCGRGHNVLRQTRVERCHCRF 368	
QY	134	RWCLXSICSDLK 145	
Db	369	HWCCYVLCDECK 380	

  

RESULT 10			
ITBI MOUSE			
ID	ITBI MOUSE	STANDARD;	PRT; 798 AA.
AC	P09055;		
DT	01-NOV-1988 (Rel. 09, Created)		
DT	01-NOV-1988 (Rel. 09, last sequence update)		
DT	15-MAR-2004 (Rel. 43, last annotation update)		
DE	Integrin beta-1 precursor (Fibronectin receptor beta subunit)		
DE	(CD29 antigen) (Integrin VLA-4 beta subunit).		
GN	ITGB1		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI	TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/c;		
RX	MEDLINE=89005707; PubMed=3262537;		
RA	Tominaga S.;		
RT	"Murine mRNA for the beta-subunit of integrin is increased in		
RT	BALB/c-3T3 cells entering the G1 phase from the G0 state.";		
RL	FEBS Lett. 238:315-319(1988).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahay J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,		
RA	Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[3]		
RP	SEQUENCE OF 2-798 FROM N.A.		
RC	STRAIN=BALB/c;		
RX	MEDLINE=89235580; PubMed=25231953;		
RA	Holers V.M., Ruff T.G., Parks D.L., McDonald J.A., Ballard L.L.,		
RA	Brown E.J.;		
RT	"Molecular cloning of a murine fibronectin receptor and its		
RT	expression during inflammation. Expression of VLA-5 is increased in		
RT	activated peritoneal macrophages in a manner discordant from major		

RT histocompatibility complex class II.";  
 RL J. Exp. Med. 169:1589-1605 (1989).  
 CC -1- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-1  
 CC 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-  
 CC 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED  
 CC SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-  
 CC 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-  
 CC 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR  
 CC FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN  
 CC THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.  
 CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN  
 CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1  
 CC ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR  
 CC FOR VCAM1 AND RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN  
 CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND  
 CC OSTEOPOINTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-I IN  
 CC CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLINIGRIN  
 CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR  
 CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A  
 CC WIDE ARRAY OF LIGANDS.  
 CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Beta-1  
 CC associates with either alpha-1, alpha-2, alpha-3, alpha-4,  
 CC alpha-5, alpha-6, alpha-7, alpha-8, alpha-9, alpha-10, alpha-11 or  
 CC alpha-V. Interacts with FLNA and FLNB (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the integrin beta chain family.  
 CC -1- SIMILARITY: Contains 2 VWFA-like domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; Y00769; CAA68738.1; -.  
 CC EMBL; BC050906; AAH50906.1; -.  
 CC EMBL; X15202; CAA33272.1; -.  
 CC PIR; PL0104; IJMSRF.  
 CC PIR; S01659; S01659.  
 CC HSPG; P05106; IJ02.  
 CC MGD; MGI:96610; Itgbl.  
 CC GO; GO:0005886; C:plasma membrane; IDA.  
 CC InterPro; IPR006209; EGF like.  
 CC InterPro; IPR002369; Integrin B.  
 CC InterPro; IPR001169; Integrin\_beta\_C.  
 CC InterPro; IPR003659; Plexin-like.  
 CC InterPro; IPR02035; VWF\_A.  
 CC Pfam; PF00362; integrin\_B; 1.  
 CC ProDom; PD01811; IntegrinB.  
 CC PRINTS; PR01186; IntegrinB.  
 CC SMART; SM00187; INB; 1.  
 CC SMART; SM00423; PSI; 1.  
 CC SMART; SM00327; VWA; 1.  
 CC PROSITE; PS00243; INTEGRIN\_BETA; 3.  
 CC PROSITE; PS00022; EGF\_1; UNKNOWN 2.  
 CC Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;  
 CC Repeat; Signal; Phosphorylation.  
 CC SIGNAL 1 20  
 CC CHAIN 21 798 INTEGRIN BETA-1.  
 CC DOMAIN 21 728 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 729 751 POTENTIAL.  
 CC DOMAIN 752 798 CYTOPLASMIC (POTENTIAL).  
 CC DOMAIN 140 378 VWA-LIKE.  
 CC DOMAIN 466 635 4 CYSTEINE-RICH TANDEM REPEATS.  
 CC REPEAT 466 515 I.  
 CC REPEAT 516 559 III.  
 CC REPEAT 560 598 III.  
 CC REPEAT 599 635 IV.  
 CC REPEAT 27 464 BY SIMILARITY.  
 CC DISULFID 27 464 BY SIMILARITY.  
 CC DISULFID 35 45 BY SIMILARITY.  
 CC DISULFID 38 75 BY SIMILARITY.

FT DISULFID 48 64 BY SIMILARITY.  
 FT DISULFID 207 213 BY SIMILARITY.  
 FT DISULFID 261 301 BY SIMILARITY.  
 FT DISULFID 401 415 BY SIMILARITY.  
 FT DISULFID 435 691 BY SIMILARITY.  
 FT DISULFID 462 466 BY SIMILARITY.  
 FT DISULFID 477 489 BY SIMILARITY.  
 FT DISULFID 486 525 BY SIMILARITY.  
 FT DISULFID 491 500 BY SIMILARITY.  
 FT DISULFID 502 516 BY SIMILARITY.  
 FT DISULFID 531 536 BY SIMILARITY.  
 FT DISULFID 533 568 BY SIMILARITY.  
 FT DISULFID 538 553 BY SIMILARITY.  
 FT DISULFID 555 560 BY SIMILARITY.  
 FT DISULFID 574 579 BY SIMILARITY.  
 FT DISULFID 576 607 BY SIMILARITY.  
 FT DISULFID 581 590 BY SIMILARITY.  
 FT DISULFID 592 599 BY SIMILARITY.  
 FT DISULFID 613 618 BY SIMILARITY.  
 FT DISULFID 615 661 BY SIMILARITY.  
 FT DISULFID 620 630 BY SIMILARITY.  
 FT DISULFID 633 636 BY SIMILARITY.  
 FT DISULFID 640 649 BY SIMILARITY.  
 FT DISULFID 646 723 BY SIMILARITY.  
 FT DISULFID 783 783 BY SIMILARITY.  
 FT MOD RES 783 783 PHOSPHORYLATION (BY SIMILARITY).  
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 363 363 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 520 520 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 584 584 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 385 385 E -> P (IN REF. 3).  
 FT CONFLICT 392 392 G -> A (IN REF. 3).  
 FT CONFLICT 443 445 IXI -> HSKL (IN REF. 3).  
 SQ SEQUENCE 798 AA; 88231 MW; 26788F7F0A168B56 CRC64;  
 Query Match 7.9%; Score 84; DB 1; Length 798;  
 Best Local Similarity 26.8%; Pred. No. 2.2;  
 Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;  
 QY 26 DTEESYSDWGLHRLGSP-ESVSNYSFDSFLLELLGGKNGVCOYRCRGKAPMPRGYKPOE 84  
 DB 543 NTNEIYS-----GKFCEDNFNCDNRSLGCGNGVC--RCRVCE-----560  
 QY 85 PNGCGSYFLGLKVPESMDLG--IPAMTKCNQLDVCYDTGANKVRC-DAKFRWCLXSTC 141  
 DB 581 ---CYPNTGSACDCSLDTGPCLANSGQICNGRGIC--ECGACK--CTDPKQ---GPTC 630  
 QY 142 SLDKRSLGFSVKVRCDSIVDTVNTVTLTGCRPPNWSQRAACICAE 189  
 DB 631 ETCQTCGLGVCAEHKEC-----VQCRAF-NKGEKKTCAQE 664  
 RESULT 11  
 FBL4\_HUMAN  
 ID FBL4\_HUMAN STANDARD; PRT; 443 AA.  
 AC Q95967; O75967;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE EGF-containing fibulin-like extracellular matrix protein 2 precursor  
 DE (Fibulin-4) (FBLN-4) (UPH1 protein) (UNQ200/PRO226).  
 GN EFEMP2 OR FBLN4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxId=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Melanoma;  
RX MEDLINE=20068041; PubMed=10601734;  
RA Giltay R., Timpl R., Koska G.;  
RT "Sequence, recombinant expression and tissue localization of two novel  
RT extracellular matrix proteins, fibulin-3 and fibulin-4.";  
RL Matrix Biol. 18:469-480(1999).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP Zemel R., Shaul Y.;  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=20435063; PubMed=10982184;  
RA Katsanis N., Venable S., Smith J.R., Lupski J.R.;  
RT "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene  
RT from the multiple retinopathy critical region on 11q13.";  
RL Hum. Genet. 106:66-72(2000).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=22867296; PubMed=12975309;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [5]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Mazza M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the fibulin family.  
CC -!- SIMILARITY: Contains 6 EGF-like domains.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AJ132819; CAAL10791.2; -

DR EMBL; AF093119; AAC62108.1; -.  
DR EMBL; AF109121; AAF65188.1; -.  
DR EMBL; AY358899; AAG9258.1; -.  
DR EMBL; BC010456; AAH10456.1; -.  
DR HSSP; P35555; 1EMN;  
DR Genew; HGNC:3219; EFEMP2.  
DR MIM; 604633; -.  
DR GO; GO:0005604; C:basement membrane; TAS.  
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_s.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR001491; Thrbomodulin.  
DR Pfam; PF00008; EGF; 4.  
DR PRINTS; PRO0907; THRBOMODULN.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS00026; EGF\_3; 4.  
DR PROSITE; PS01187; EGF\_CA; 6.  
DR Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.  
FT SIGNAL 1 25 POTENTIAL  
FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR  
FT DOMAIN 36 81 MATRIX PROTEIN 2.  
FT DOMAIN 123 163 EGF-LIKE 1, DIVERGENT.  
FT DOMAIN 164 202 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 203 242 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 243 282 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 283 328 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
FT DISULFID 127 140 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
FT DISULFID 134 149 BY SIMILARITY.  
FT DISULFID 151 162 BY SIMILARITY.  
FT DISULFID 168 177 BY SIMILARITY.  
FT DISULFID 173 186 BY SIMILARITY.  
FT DISULFID 188 201 BY SIMILARITY.  
FT DISULFID 207 217 BY SIMILARITY.  
FT DISULFID 213 226 BY SIMILARITY.  
FT DISULFID 228 241 BY SIMILARITY.  
FT DISULFID 247 258 BY SIMILARITY.  
FT DISULFID 254 267 BY SIMILARITY.  
FT DISULFID 269 281 BY SIMILARITY.  
FT DISULFID 287 300 BY SIMILARITY.  
FT DISULFID 294 309 BY SIMILARITY.  
FT DISULFID 315 327 BY SIMILARITY.  
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 5 5 A -> T (IN REF. 1).  
FT CONFLICT 44 51 EWDPSQH -> TOTAN (IN REF. 2).  
FT CONFLICT 103 111 ACHNPPCP -> VNTQPLET (IN REF. 2).  
FT CONFLICT 294 294 C -> W (IN REF. 2).  
FT CONFLICT 354 356 RSV -> AER (IN REF. 2).  
FT CONFLICT 355 355 S -> R (IN REF. 3).  
FT SEQUENCE 443 AA; 49391 MW; 9E9AC2393780D3B8 CRC64;  
SQ  
Query Match 7.8%; Score 83.5; DB 1; Length 443;  
Best Local Similarity 21.8%; Pred. No. 1.2;  
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;  
QY 6 GFVLW-----LSLGGGLAQSDTSPDTEESYSD---W--GLRHRL-----GSF 43  
DB 10 GSLLWALLLLGLGASPDSEPDSTYCTDGYEWDPSQCHRDVNECLTPEACKGEM 69  
QY 44 ESNVSFDSFLELLGKNGVCQYRC-----RYGKAPMP-----RPGYKP 82  
DB 70 KCHNY-----GG-----YLCPRSAVINDLHGEGPPPPVPAQHPNCPGYP 115  
QY 83 QEPNGCGSYFLGLKPESMDLGPAMTKC-----CNQLDVCYDTGANKYR-----C--- 129  
DB 116 DDQDSC-----VDVDECAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDI 165  
QY 130 -DAKFRWCLXISCDLKRSL-----GF-----VSKVEACD---SLVDVTNTVNTWL 171

```
Db 166 DCRVRYQHR-CVNLPGSRQCCEPGLGPNRSCVDVNECDMGAPCEQRCSNSYCTF 224
QY 172 GCR 174
Db 225 LCR 227

RESULT 12
UREL_YEREN
ID UREL_YEREN STANDARD; PRT; 571 AA.
AC P31494;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
GN UREAC OR YEOC.
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2635 / Serotype O:3;
RX MEDLINE=94320783; PubMed=8045421;
RA de Koning-Ward T.P., Ward A.C., Robins-Browne R.M.;
RT "Characterisation of the urease-encoding gene complex of Yersinia
enterocolitica.";
RL Gene 145:25-32(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=6471/76 / Serotype O:3;
RX MEDLINE=93273501; PubMed=8500886;
RA Skurnik M., Batsford S., Mertz A.K.H., Schiltz E., Toivanen P.;
RT "The putative arthritogenic cationic 19-kilodalton antigen of
Yersinia enterocolitica is a urease beta-subunit.";
RL Infect. Immun. 61:2498-2504(1993).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).
CC -!- PTM: Lys-221 is carbamylated. The carbamoyl group provides the
ligands for the two nickel ions (By similarity).
CC -!- SIMILARITY: Belongs to the urease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).
CC
DR EMBL; L24101; AAA50996.1; -
DR EMBL; Z18865; CAA79316.1; -
DR FIR; S36028; S36028.
DR HSSP; P18314; 1FWF.
DR MEROPS; M38.UNW; -
DR InterPro; IPR006680; Amidohydro 1.
DR InterPro; IPR005848; Pept M38 urease.
DR InterPro; IPR008295; Urease_alpha.
DR Pfam; PF01979; Amidohydro_1; 1.
DR Pfam; PF00449; urease; 1.
DR FIRSF; FIRSF001226; Urease_alpha; 1.
DR PRINTS; PR01752; UREASE.
DR PROSITE; PS00145; UREASE_2; 1.
DR PROSITE; PS01120; UREASE_1; 1.
KW Hydrolase; Metal-binding; Nickel.
FT INIT MET 0 0 BY SIMILARITY.
FT METAL 138 138 NICKEL 2 (BY SIMILARITY).
FT METAL 140 140 NICKEL 2 (BY SIMILARITY).
FT METAL 221 221 NICKEL 1 AND 2 (BY SIMILARITY).
FT METAL 250 250 NICKEL 1 (BY SIMILARITY).
FT METAL 276 276 NICKEL 1 (BY SIMILARITY).
```

```
FT METAL 364 364 NICKEL 2 (BY SIMILARITY).
FT ACT SITE 324 324 BY SIMILARITY.
FT CONFLICT 29 30 IE -> MQ (IN REF. 2).
FT CONFLICT 66 66 V -> GY (IN REF. 2).
FT CONFLICT 68 82 DLVITNTIVDARLG -> EFSHNQRHYCCSPFR
(IN REF. 2).
FT CONFLICT 96 96 A -> V (IN REF. 2).
FT CONFLICT 114 114 M -> L (IN REF. 2).
FT CONFLICT 137 137 S -> T (IN REF. 2).
FT CONFLICT 405 405 L -> V (IN REF. 2).
FT CONFLICT 440 440 D -> V (IN REF. 2).
SQ SEQUENCE 571 AA; 60952 MW; 99C7944554FB58EA CRC64;

Query Match 7.8%; Score 83.5; DB 1; Length 571;
Best Local Similarity 25.8%; Pred. No. 1.7;
Matches 31; Conservative 17; Mismatches 49; Indels 23; Gaps 5;

QY 15 GGLAQSDTSPDTBESYSDWGLRHRLRGFSFES--VNSYFDSFLELLGGKNGVCQYRCRYGK 72
Db 160 GGGIGPTDGTNGTIVTPGPMNIQMLRSVEGLPVN-----VGILGKNS-----YGR 206
QY 73 APMRP-----GYKQPEPNGCGSYFL--GLKVPESMDLGPAMTKCCNQLDVCYDTGCA 124
Db 207 GPLELQAIAGVVGKVEDWGTATNALRHSLRMADEMDIQSVHTDSLNECGYVEDTIDA 266

RESULT 13
WN1B_HUMAN
ID WN1B_HUMAN STANDARD; PRT; 389 AA.
AC O00744; O00747; O8WZ97;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Wnt-10b protein precursor (Wnt-12).
GN WNT10B OR WNT12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97430838; PubMed=9284937;
RA Hardiman G., Kastelein R.A., Bazan J.F.;
RT "Isolation, characterization and chromosomal localization of human
WNT10B.";
RL Cytogenet. Cell Genet. 77:278-282(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21570122; PubMed=11713588;
RA Saitoh T., Kirikoshi H., Mine T., Katoh M.;
RT "Proto-oncogene WNT10B is up-regulated by tumor necrosis factor alpha
in human gastric cancer cell line MKN45.";
RL Int. J. Oncol. 19:1187-1192(2001).
RN [3]
RP SEQUENCE OF 45-347 FROM N.A.
RX TISSUE=Fetal brain;
RX MEDLINE=97236668; PubMed=9121776;
RA Bui T.D., Rankin J., Smith K., Huguet E.L., Ruben S., Strachan T.,
RA Harris A.L., Lindsay S.;
RT "A novel human Wnt gene, WNT10B, maps to 12q13 and is expressed in
human breast carcinomas.";
RL Oncogene 14:1249-1253(1997).
RN [4]
RP SEQUENCE OF 253-368 FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=98110581; PubMed=9441749;
RA Bergstein I., Eisenberg L.M., Bhallerao J., Jenkins N.A.,
RA Copeland N.G., Osborne M.P., Bowcock A.M., Brown A.M.C.;
RT "Isolation of two novel Wnt genes, WNT14 and WNT15, one of which
(WNT15) is closely linked to WNT3 on human chromosome 17q21.";
RL Genomics 46:450-458(1997).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors. Probable developmental protein. May be a
```



CC signaling molecule which affects the development of discrete  
CC regions of tissues. Is likely to signal over only few cell  
CC diameters (By similarity).  
CC  
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the  
CC extracellular matrix.  
CC  
CC -!- TISSUE SPECIFICITY: DETECTED IN MOST ADULT TISSUES. HIGHEST LEVELS  
CC WERE FOUND IN HEART AND SKELETAL MUSCLE. LOW LEVELS ARE FOUND IN  
CC BRAIN.  
CC  
CC -!- DEVELOPMENTAL STAGE: INFANT BRAIN HAS HIGHER LEVELS OF WNT10B THAN  
CC ADULT BRAIN.  
CC  
CC -!- SIMILARITY: Belongs to the Wnt family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U81787; AAB51695.1; -;  
CC EMBL; A8070724; BAB72181.1; -;  
CC EMBL; X97057; CAA65769.1; -;  
CC EMBL; AF028700; AAC39549.1; -;  
CC Genew; HGNC:12775; WNT10B.  
CC MIM; 601906; -;  
CC InterPro; IPR005817; Wnt.  
CC InterPro; IPR005816; Wnt\_grthfactor.  
CC Pfam; PF00110; wnt; 1.  
CC PRINTS; PR01349; WNTPROTEIN.  
CC SMART; SM00097; WNT1; 1.  
CC PROSITE; PS00246; WNT1; 1.  
CC Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.  
CC  
CC SIGNAL 1 28 POTENTIAL.  
CC  
CC FT CHAIN 29 389 WNT-10B PROTEIN.  
CC FT CARBOHYD 93 93 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC FT CARBOHYD 335 335 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC FT CONFLICT 60 60 G -> D (IN REF. 1).  
CC FT CONFLICT 149 149 K -> R (IN REF. 3).  
CC FT CONFLICT 295 295 P -> S (IN REF. 3).  
CC FT CONFLICT 311 311 F -> L (IN REF. 3).  
CC  
CC SQ SEQUENCE 389 AA; 43000 MW; F973F2CA0DB115EF CRC64;  
  
Query Match 7.7%; Score 82.5; DB 1; Length 389;  
Best Local Similarity 21.2%; Pred. No. 1.4;  
Matches 28; Conservative 16; Mismatches 41; Indels 47; Gaps 5;  
  
QY 59 GKNVGVQYRCRYGKAMPKPR-----PGYKQPNPNCGSY 91  
Db 251 GTSGSCQFKTCRAAPEFAVGAALRERLGRAIFIDTHNRNSGAFQPLRPRLSGELVY 310  
  
QY 92 FLGLKVPESMD---LGIPAMT-KCNQLDVCYDTGCA-----NKYRCDAKF 133  
Db 311 F--EKSPDFCERDPTMGSPGTRACNKTSLRLDGCGLCCGSHNVLRQTRVERCHCRF 368  
  
QY 134 RWCLXSICSDLK 145  
Db 369 HMCYVLCDECK 380  
  
RESULT 14  
URE1 YERPS STANDARD; PRT; 571 AA.  
AC P52313;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).  
GN UREAC.  
OS Yersinia pseudotuberculosis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=633;

RN SEQUENCE FROM N.A.  
RP STRAIN=IP 2777;  
RC MEDLINE=97270511; PubMed=9125594;  
RX Riott B., Berche P., Simonet M.;  
RA "Urease is not involved in the virulence of Yersinia  
RT pseudotuberculosis in mice."  
RL Infect. Immun. 65:1985-1990(1997).  
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
CC -!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).  
CC -!- SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).  
CC -!- PTM: Lys-221 is carbamylated. The carbamoyl group provides the  
CC ligands for the two nickel ions (By similarity).  
CC -!- SIMILARITY: Belongs to the urease family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U40842; AAB87854.1; -;  
CC HSSP; P18314; 1FWF.  
CC MEROPS; M38.UNW; -;  
CC InterPro; IPR006680; Amidohydro 1.  
CC InterPro; IPR005848; Pept\_M38\_urease.  
CC InterPro; IPR008295; Urease\_alpha.  
CC Pfam; PF01979; Amidohydro\_1; 1.  
CC Pfam; PF00449; urease; 1.  
CC PRINTS; PIRSF001226; Urease\_alpha; 1.  
CC PRINTS; PR01752; UREASE.  
CC PROSITE; PS00145; UREASE\_2; 1.  
CC PROSITE; PS01200; UREASE\_1; 1.  
CC Hydrolase; Metal-binding; Nickel.  
CC INIT MET 0 0 BY SIMILARITY.  
CC FT METAL 138 138 NICKEL 2 (BY SIMILARITY).  
CC FT METAL 140 140 NICKEL 2 (BY SIMILARITY).  
CC FT METAL 221 221 NICKEL 1 AND 2 (BY SIMILARITY).  
CC FT METAL 250 250 NICKEL 1 (BY SIMILARITY).  
CC FT METAL 276 276 NICKEL 1 (BY SIMILARITY).  
CC FT METAL 364 364 NICKEL 2 (BY SIMILARITY).  
CC FT ACT SITE 324 324 BY SIMILARITY.  
CC SQ SEQUENCE 571 AA; 60874 MW; 88B6056FA16F89CC CRC64;  
  
Query Match 7.6%; Score 81.5; DB 1; Length 571;  
Best Local Similarity 25.0%; Pred. No. 2.6;  
Matches 30; Conservative 18; Mismatches 49; Indels 23; Gaps 5;  
  
QY 15 GGGIAQSDTSPTTESYSDWGLRHLRGSFES--VNSYFDSFLELLGGKNGVCOYCRYGK 72  
Db 160 GGGIGFTDGTNGTSVTPGPWNIQMLRSIEGLPVN-----VGILKGNKNS-----YGR 206  
  
QY 73 AMPRP-----GYKQPNPNCGSYEL--GLKVPESMDLGIPIAMTKCNQLDVCYDTGCA 124  
Db 207 GPLLEQAIAGVGVYKVHEDWGATANALRALHRADEVDIQSVVHTDSLNECGYVEITIDA 266  
  
RESULT 15  
IBP2\_RAT STANDARD; PRT; 304 AA.  
AC P12843;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Insulin-like growth factor binding protein 2 precursor (IGFBP-2)  
DE (IBP-2) (IGF-binding protein 2) (BRL-BP).  
GN IGFBP2 OR IGFBP-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=101116;



RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=89174801; PubMed=2538475;  
RA Brown A.L., Chiarlotti L., Orlovski C.C., Mehlman T., Burgers W.H.,  
RA Ackerman E.J., Bruni C.B., Rechler M.M.;  
RT "Nucleotide sequence and expression of a cDNA clone encoding a fetal  
RT rat binding protein for insulin-like growth factors.";  
RL J. Biol. Chem. 264:5148-5154(1989).  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=90014825; PubMed=2477691;  
RA Margot J.B., Binkert C., Mary J.-L., Landwehr J., Heinrich G.,  
RA Schwaner J.;  
RT "A low molecular weight insulin-like growth factor binding protein  
RT from rat: cDNA cloning and tissue distribution of its messenger  
RT RNA.";  
RL Mol. Endocrinol. 3:1053-1060(1989).  
RN  
RP SEQUENCE OF 38-68.  
RX MEDLINE=86278218; PubMed=2426267;  
RA Mottola C., Macdonald R.G., Brackett J.L., Mole J.E., Anderson J.K.,  
RA Czech M.P.;  
RT "Purification and amino-terminal sequence of an insulin-like growth  
RT factor-binding protein secreted by rat liver BRL-3A cells.";  
RL J. Biol. Chem. 261:11180-11188(1986).  
RN  
RP SEQUENCE OF 35-64.  
RC TISSUE=Sera;  
RX MEDLINE=89073708; PubMed=2480123;  
RA Shimomura M., Schroeder R., Shimasaki S., Ling N.;  
RT "Identification of a novel binding protein for insulin-like growth  
RT factors in adult rat serum.";  
RL Biochem. Biophys. Res. Commun. 165:189-195(1989).  
RN  
RP SEQUENCE OF 178-204.  
RX MEDLINE=89076308; PubMed=2974285;  
RA Wang J.F., Hampton B., Mehlman T., Burgess W.H., Rechler M.M.;  
RT "Isolation of a biologically active fragment from the carboxy  
RT terminus of the fetal rat binding protein for insulin-like growth  
RT factors.";  
RL Biochem. Biophys. Res. Commun. 157:718-726(1988).  
CC -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs  
CC and have been shown to either inhibit or stimulate the growth  
CC promoting effects of the IGFs on cell culture. They alter the  
CC interaction of IGFs with their cell surface receptors.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MISCELLANEOUS: Binds IGF-II more than IGF-I.  
CC -!- SIMILARITY: Contains 1 IGFBP domain.  
CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC ENBL; J04486; AAA0829.1; -;  
CC ENBL; M58559; -; NOT\_ANNOTATED\_CDS.  
CC ENBL; M31672; AAA1381.1; -;  
CC PIR; A33274; A33274.  
CC HSSP; P24593; IBOE.  
CC InterPro; IPR009030; Grow\_fac\_recep.  
CC InterPro; IPR008867; Insl\_gro\_fac\_pr.  
CC InterPro; IPR000716; Thyroglobulin\_1.  
CC Pfam; PF00219; IGFBP; 1.  
CC Pfam; PF00886; thyroglobulin\_1; 1.  
CC PIRSF; PIRSF001969; IGFBP1-6; 1.  
CC SMART; SM00121; IB; 1.  
CC SMART; SM00211; TY; 1.  
CC PROSITE; PS00222; IGF\_BINDING; 1.

DR PROSITE; PS00484; THYROGLOBULIN\_1; 1.  
KW Growth factor binding; Signal.  
FT SIGNAL 1 34  
FT CHAIN 35 304 INSULIN-LIKE GROWTH FACTOR BINDING  
FT DOMAIN 236 285 THYROGLOBULIN TYPE-I.  
FT SITE 280 282 CELL ATTACHMENT SITE.  
FT CONFLICT 298 298 V -> A (IN REF. 2).  
SQ SEQUENCE 304 AA; 32883 MW; 8558B7E2C915348F CRC64;  
  
Query Match 7.6%; Score 80.5; DB 1; Length 304;  
Best Local Similarity 22.5%; Pred. No. 1.6;  
Matches 39; Conservative 25; Mismatches 60; Indels 49; Gaps 9;  
  
QY 26 DTEESYSDWGLRHLRGSPESVNSYFDSLELLGGKNGVCQYRCYKAPMPRGYK--- 81  
Db 129 DSEDDHSEGL-----VENHVDGTMNMGSSA-----GRKP-PKSGMKELAV 170  
  
QY 82 -----POEPNGCGSYFGLKVPESMDLIGIPATKCCNQLDVCYDTCCGANKYRCDAKER 134  
Db 171 PREKYNQHRQMGKAKHLSEEPKKL-RPPPARTPCQQLDQVLERISTMLPDD---R 226  
  
QY 135 WCLXICSDLKRSLSGVSKVEACDSLVDTVFNVTWL-GCRPFMNSORAAIC 186  
Db 227 GPLEHLYS-----LHFPNCDK-----HGLYNLKQCKMSLNGQGEWC 264  
  
Search completed: May 17, 2004, 10:42:46  
Job time : 19 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:39:44 ; Search time 45 Seconds  
(without alignment)  
1360.234 Million cell updates/sec

Title: US-10-621-401-145  
Perfect score: 1066  
Sequence: 1 MKLAGFLVWLSLGGGLAQ.....PFMNSQRAACICAEKEEL 194

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

- SPTREMBL 25.\*  
1: sp archaea.\*  
2: sp bacteria.\*  
3: sp fungi.\*  
4: sp human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	949.5	89.1	195	11 Q8VC81	Q8VC81 mus musculus
2	677	63.5	180	13 Q7ZTY1	Q7ZTY1 brachydanio
3	465	43.6	205	11 Q8BMX2	Q8BMX2 mus musculus
4	441.5	41.4	242	13 Q7ZV17	Q7ZV17 brachydanio
5	230	21.6	230	5 Q9VUV6	Q9VUV6 drosophila
6	186	17.4	114	5 Q8XC7	Q8XC7 drosophila
7	96.5	9.1	234	5 Q9BL06	Q9BL06 caenorhabdi
8	87.5	8.2	1037	2 Q8VLQ3	Q8VLQ3 alteromonas
9	86.5	8.1	281	5 Q8SXC6	Q8SXC6 drosophila
10	86.5	8.1	342	5 Q9W410	Q9W410 drosophila
11	85.5	8.0	1054	16 Q87HX4	Q87HX4 vibrio para
12	84.5	7.9	117	5 Q8M050	Q8M050 caenorhabdi
13	84	7.9	798	11 Q8BTU0	Q8BTU0 mus musculus
14	83.5	7.8	443	4 Q96TF5	Q96TF5 homo sapien
15	83.5	7.8	854	16 Q87HH8	Q87HH8 vibrio para
16	83.5	7.8	1053	2 Q8KRL3	Q8KRL3 vibrio harv

17	82	7.7	1070	16 Q8D7E1	Q8D7E1 vibrio vuln
18	82	7.7	1289	5 Q86AC3	Q86AC3 dictyosteli
19	81	7.6	2192	5 Q01768	Q01768 caenorhabdi
20	80.5	7.6	443	11 Q9JMO6	Q9JMO6 mus musculus
21	80.5	7.6	1051	16 Q9KLP3	Q9KLP3 vibrio chol
22	80.5	7.6	1526	10 Q7XW03	Q7XW03 oryza sativ
23	80	7.5	414	10 Q9SH19	Q9SH19 arabidopsis
24	80	7.5	553	12 Q83536	Q83536 measles vir
25	80	7.5	553	12 Q83533	Q83533 measles vir
26	80	7.5	632	5 Q9VFN3	Q9VFN3 drosophila
27	80	7.5	822	11 Q62287	Q62287 mus musculu
28	79.5	7.5	317	6 Q97599	Q97599 bos taurus
29	79.5	7.5	443	4 Q9H3D5	Q9H3D5 homo sapien
30	79.5	7.5	1241	5 Q9U144	Q9U144 leishmania
31	79.5	7.5	1704	5 Q94446	Q94446 chironomus
32	79	7.4	419	5 Q8IOM3	Q8IOM3 giardia lam
33	79	7.4	446	11 Q8BV23	Q8BV23 mus musculu
34	79	7.4	504	11 Q8BZT7	Q8BZT7 mus musculu
35	79	7.4	621	2 Q9F486	Q9F486 alteromonas
36	79	7.4	621	2 Q53401	Q53401 alteromonas
37	79	7.4	692	16 Q8A6D1	Q8A6D1 bacteroides
38	79	7.4	712	5 Q20323	Q20323 caenorhabdi
39	78.5	7.4	1821	4 Q14767	Q14767 homo sapien
40	78.5	7.4	2189	5 Q9BI05	Q9BI05 eimeria ten
41	78	7.3	177	5 Q8IML0	Q8IML0 drosophila
42	78	7.3	411	16 Q8CXW6	Q8CXW6 escherichia
43	78	7.3	638	4 Q8N8H6	Q8N8H6 homo sapien
44	78	7.3	710	11 Q91VP4	Q91VP4 mus musculu
45	78	7.3	710	11 Q61898	Q61898 mus musculu

#### ALIGNMENTS

#### RESULT 1

Q8VC81  
ID Q8VC81 PRELIMINARY; PRT; 195 AA.  
AC Q8VC81;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE RIKEN cDNA 2010002E04 gene.  
GN 2010002E04RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC021592; AAH21592.1; -;  
DR MGD; MGI:1917086; 2010002E04RIK.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR000886; ER\_target\_S  
DR InterPro; IPR001211; PhospholipaseA2.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
SQ SEQUENCE 195 AA; 21722 MW; 83A9E656ED08DA24 CRC64;

Query Match 89.1%; Score 949.5; DB 11; Length 195;  
Best Local Similarity 89.2%; Pred. No. 5.8e-96;  
Matches 174; Conservative 3; Mismatches 17; Indels 1; Gaps 1;  
QY 1 MKLAGFLVWLSLGGGLAQSDTSPDTEESYSDWGLRHRLRGFSFVSNSYDFSLGLGK 60  
Db 1 MKLCCFFLLWLGVLGNLAQSDPSPKEESYSDWGLRQLRGFSFVSNSYVDSFMLGK 60  
QY 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCCSYFLGLKVPESMDLGIIPAMTKCCNQLDVCYD 120  
Db 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCCSYFLGLKVPESMDLGIIPAMTKCCNQLDVCYD 120

```

QY 121 TCGANKYRCDAKFRCLXSCDLKRSGLGFSKYVE-ACDSLVDVTVENTVTLGCRPFMNS 179
DB 121 TCGANKYRCDAKFRCLXSCDLKRSGLGFSVNSVEAACDSLADTVENTVTLGCRPFMNS 180

QY 180 QRAACICAAEEKEEL 194
DB 181 QRAACICAAEEKEEL 195

RESULT 2
Q7ZTV1
ID Q7ZTV1 PRELIMINARY; PRT; 180 AA.
AC Q8BMX2;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to phospholipase A2, group XIII.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2238257; PubMed=12477932;
RA Klausner R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052113; AAH52113.1; --
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR000886; ER target S.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS000144; ER_TARGET; 1.
SQ SEQUENCE 180 AA; 19975 MW; F44C2620E690A601 CRC64;

Query Match 63.5%; Score 677; DB 13; Length 180;
Best Local Similarity 67.6%; Pred. No. 4.3e-66;
Matches 115; Conservative 23; Mismatches 26; Indels 6; Gaps 2;

QY 27 TBESY--SMGLRHURGSPESVNSYFDSFLELLGKNGVCQYRCYRKAPMPRGYKPOE 84
DB 15 TBESDDDDWGFGRGSLQSYNGVYFDSFLELLGKNGVGRDGVQCFRCYRKAPMPRGYQMS 74

QY 85 PNGCGSYFLGLKVPESMDLIGIPAMTKCCNQLDVCYDTCCGANKYRCDAKFRWCLXSCDL 144
DB 75 PDGCSYLLGFGQ-----FDMGVFAMTKCCNQLDVCYETCGSNKYRCUTKFRWCLXSCDL 130

```

```

QY 145 KRSGLGFSKYVEACDSLVDVTVENTVTLGCRPFMNSQRAACICAAEEKEEL 194
DB 131 KXSLGLMSKYVEACETTFADTWTNTVTLGCRPFMNGQRAASCYCEGEKDEL 180

RESULT 3
Q8BMX2
ID Q8BMX2 PRELIMINARY; PRT; 205 AA.
AC Q8BMX2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Group XII-1 phospholipase A2 (Fragment).
GN PLA2G12 OR 2310004B05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK012414; BAC25368.1; --
DR MGB; MGI:1913600; Pla2g12.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.
FT NON TER 1
SQ SEQUENCE 205 AA; 22495 MW; 040FRAEEF01DE691 CRC64;

Query Match 43.6%; Score 465; DB 11; Length 205;
Best Local Similarity 43.9%; Pred. No. 9.5e-43;
Matches 83; Conservative 42; Mismatches 50; Indels 14; Gaps 3;

QY 8 IYVWLMSLGGHQAQSDTSPDTESYSDW--GLRHURGSPESVNSYFDSFLELLGKNGVCQ 65
DB 29 LLLLIATARGOEQDT-----PDWRATLKTIRNGIHKIDTYLNAALDLGGEDGLCQ 80

QY 66 YRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLIGIPAMTKCCNQLDVCYDTCCGAN 125
DB 81 YKSDGSKPVPYRGYKPSPPNGCGSPFGV---HLNIGIFSLTKCCNQHRCVETCKS 136

QY 126 KYRCDKFRWCLXSCDLKRSGLGFSKYVEACDSLVDVTVENTVTLGCRPFMNSQRAACI 185
DB 137 KNDCEEFOYCLSKICRDVQKTGLSQNVQACETTVLLFDSVHLGCKPYLDQSRAACW 196

QY 186 CAEEKEEL 194
DB 197 CRYEKTDL 205

RESULT 4
Q7ZV17
ID Q7ZV17 PRELIMINARY; PRT; 242 AA.
AC Q7ZV17;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.

```

```
RC TISSUE=Body;
RA Strauberg B.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046040; AAH46040.1; -.
DR GO; 0005509; F:calcium ion binding; IEA.
DR GO; 0004623; F:phospholipase A2 activity; IEA.
DR GO; 0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 242 AA; 27313 MW; 0383D3FC147B9FE4 CRC64;

Query Match 41.4%; Score 441.5; DB 13; Length 242;
Best Local Similarity 42.3%; Pred. No. 4.4e-40;
Matches 82; Conservative 34; Mismatches 63; Indels 15; Gaps 3;

OY 3 LASGFLVLSIGGGLAQSDTSPDTEESYSDV--GLRHLRGSFESVNSYFDSFLELLGK 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 LLSGLV-----LSTKADGSDDEIKPPDWRKTINGIRSGIHRIDKYLNNALDLIGGS 112
OY 61 NGVCYRCYKAMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 DQCQFTCGDGYTPERNYRPPPPNGCGSPUGFGQ----FDVGIPSMTRCCNEHRCYD 168
OY 121 TCGANKYRCDAKFRWCLXSIKSLKSLGFSVKEACDSLVDTVFTVMTLGCRCPFMSQ 180
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
169 SCGRKSDCDEGFQCLNICQNLQWTLGSLSVQACESAVTLVDTVWHLGCKYFLDSQ 228
OY 181 RAACICAEKEEKEEL 194
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
229 RSACICHVEEKPD 242

RESULT 5
O9VUV6 PRELIMINARY; PRT; 230 AA.
AC O9VUV6; Q9BIV5;
DT 01-MAY-2000 (TrEMBLrel. 12, Created)
DT 01-OCT-2002 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG17035 protein (Group XIV secreted phospholipase A2).
GN GXIVSPLA2 OR CG17035.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Housoun K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
```

```
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuakern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Man K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McKintosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Takahashi K.;
RT "Cloning of Drosophila group XIV secreted phospholipase A2."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003529; AAF49567.2; -.
DR EMBL; AF349541; AAK30169.1; -.
DR FlyBase; Fgn0036545; GXIVSPLA2.
DR GO; 0005509; F:calcium ion binding; IEA.
DR GO; 0004623; F:phospholipase A2 activity; IEA.
DR GO; 0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.
DR SEQUENCE 230 AA; 25952 MW; 925882C6D32F3466 CRC64;
SQ
```

Query Match 21.6%; Score 230; DB 5; Length 230;  
Best Local Similarity 30.8%; Pred. No. 6.9e-17;  
Matches 60; Conservative 31; Mismatches 50; Indels 54; Gaps 11;

SVIRSKAS R., TECTOR C., TURNER R., VENTER E., WANG A.H., WANG X.,  
WANG Z.Y., WASAMAN D.A., WEINSTOCK G.M., WEISENBACH J.,  
WILLIAMS S.M., WOODGATE, WORLEY K.C., WU D., YANG S., YAO Q.A., YE J.,  
YEH R.F., ZAVERI J.S., ZHAN M., ZHANG G., ZHAO Q., ZHENG L.,  
ZHENG X.H., ZHONG F.N., ZHONG W., ZHOU X., ZHU S., ZHU X., SMITH H.O.,  
GIBBS R.A., MYERS E.W., RUBIN G.M., VENTER J.C.;  
"The genome sequence of *Drosophila melanogaster*.";  
Science 287:2185-2195 (2000).  
[3]  
SEQUENCE FROM N.A.  
CELNIKER S.E., ADAMS M.D., KRONMILLER B., WAN K.H., HOIT R.A.,  
EVANS C.A., GOCAYNE J.D., AMANATIDES P.G., BRANDON R.C., ROGERS Y.,  
BANSON J., AN H., BALDWIN D., BANSON J., BEESON K.Y., BUSAM D.A.,  
CARLSON J.W., CENTER A., CHAMPE M., DAVENPORT L.B., DIETZ S.M.,  
DODSON K., DORSETT V., DOUP L.E., DOYLE C., DRESNEK D., FARFAN D.,  
FERRIERA S., FRISE E., GALLE R.F., GAIG N.S., GEORGE R.A.,  
GONZALEZ M., HOUCK J., HOSKINS R.A., HOSTIN D., HOWLAND T.J.,  
IBEGWAM C., JALALI M., KRUSE D., LI P., MATTEI B., MOSHREFI A.,  
MCINTOSH T.C., MOY M., MURPHY B., NELSON C., NELSON K.A., NUNOO J.,  
PACLEB J., PARAGVAS V., PARK S., PATEL S., PFEIFER B.,  
PHOUANANAVONG S., PITTMAN G.S., PURI V., RICHARDS S., SCHEELER F.,  
STAPLETON M., STRONG R., SVIRSKAS R., TECTOR C., TYLER D.,  
WILLIAMS S.M., ZAVERI J.S., SMITH H.O., VENTER J.C., RUBIN G.M.;  
"Sequencing of *Drosophila melanogaster* genome".;  
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[4]  
SEQUENCE FROM N.A.  
MISRA S., CROSBY M.A., MATTHEWS B.B., BAYRAKTAOGLU L., CAMPBELL K.,  
HRADCKY P., HUANG Y., KAMINER J.S., PROCHNICK S.E., SMITH C.D.,  
TUPY J.L., BERGMAN C., BERMAN B., CARLSON J.W., CELNIKER S.E.,  
CLAMP M., DRYSDALE R., EMERT D., FRISE E., DE GREY A., HARRIS N.,  
KRONMILLER B., MARSHALL B., MILLBURN G., RICHTER J., RUSSO S.,  
SEARLE S.M.J., SMITH E., SHU S., SMUTNIAK F., WHITFIELD E.,  
ASHBURNER M., GELBART W.M., RUBIN G.M., MUNGALL C.J., LEWIS S.E.;  
"Annotation of *Drosophila melanogaster* genome".;  
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[5]  
SEQUENCE FROM N.A.  
ADAMS M.D., CELNIKER S.E., GIBBS R.A., RUBIN G.M., VENTER C.J.;  
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

```

RN      [6]
RP      SEQUENCE FROM N.A.
RL      FlyBase;
RA      Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RE      EMBL; AY094881; AM11034.1; -.
DR      EMBL; AF003529; AAN1172.1; -.
DR      EMBL; FBN0036545; GXIVPLA2.
DR      FlyBase; FBGN005509; F:calcium ion binding; IEA.
DR      GO; GO:0005509; F:phospholipase A2 activity; IEA.
DR      GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR      GO; GO:0016042; F:lipid catabolism; IEA.
DR      InterPro; IPR001211; PhospholipaseA2.
DR      PROSITE; PS00116; FA2_HIS; 1.
DR      PROSITE; PS00116; FA2_HIS; 1.
SQ      SEQUENCE 114 AA; 13155 MW; 020303F23839E262 CRC64;

Query Match      17.4%; Score 186; DB 5; Length 114;
Best Local Similarity 37.5%; Pred.No.2e-12;
Matches 30; Conservative 16; Mismatches 34; Indels 0; Gaps 0

Qy      108 MTKCCNQLDVCYDTGCANGKRCDAKFRWCLASICSLDKRSILGFYSKVACDLSLVDVTVENT 167
Db      1 METCCNPDHICIDYTCNSDKELCDLDFKRLKYKCDSEYKSIASDLIMMGCKRAAKQLFTG 60

Qy      168 VWTLCGRPFMNSQRAACICA 187
Db      61 TLTLCGRSYLDSQQRSCYCA 80

RESULT 7
Q9BL06
ID      Q9BL06
AC      Q9BL06;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

```

```

RN
RP SEQUENCE FROM N.A.
RC
RX STRAIN=O-7;
RX MEDLINE=93106952; PubMed=8416892;
RX Tsujibo H., Orikoshi H., Tanno H., Fujimoto K., Miyamoto K., Imada C.,
RA Okami Y., Inamori Y.;
RA "Cloning, sequence, and expression of a chitinase gene from a marine
RT bacterium, Alteromonas sp. strain O-7,"
RL J. Bacteriol. 175:176-181(1993).
RL EMBL: AB063629; BAB79618.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0030246; F:carbohydrate binding; IEA.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR DR InterPro: IPR003610; CMB 5 12.
DR DR InterPro: IPR001223; Glyco hydro_18.
DR DR InterPro: IPR001579; Glyco hydro_18AS.
DR DR Pfam: PF02839; CMB 5 12; 1-.
DR DR Pfam: PF00704; Glyco_hydro_18; 1.
DR DR ProDom: PD000471; Glyco_hydro_18; 1.
DR DR SMART: SM00495; ChtBD3; 2.
DR DR SMART: SM00636; Glyco_18; 1.
DR DR PROSITE: PS01095; CHITINASE 18; 1.
DR KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 27 POTENTIAL.
SQ SEQUENCE 1037 AA; 112152 MW; EC693498B03E4324 CRC64;

Query Match 8.2%; Score 87.5; DB 2; Length 1037;
Best Local Similarity 23.9%; Pred. No. 1.9;
Matches 26; Conservative 18; Mismatches 32; Indels 33; Gaps 4;

Qy 14 LGGGLAQSDTSPDTESY-----SDWGLRHLSGFES-----VNSYFD 51
Db 569 VGHNASLFDGEISLQKNVYGTKEFG:GYLNTDWAVKYFSVAGRNIGIPIYTR 628

Qy 52 SELELLGKNGVCQYRCRYGKAPNR----PGYKPOEENGCGSYFLGL 95
Db 629 GFRDVTGTTNGL-----WGQALPNOADCPFGTSGEKKKNGANGVI 671

RESULT 9
Q8SXC6 PRELIMINARY; PRT; 281 AA.
ID Q8SXC6
AC Q8SXC6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE GH07387P.
GN CG3009.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarrin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Man K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceinlier S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY094683; AAM11036.1; -.
DR FlyBase: FBgn029720; CG3009.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004623; F:phospholipase A2 activity; IEA.
DR GO: GO:0016042; F:lipid catabolism; IEA.
DR InterPro: IPR001211; PhospholipaseA2.
DR InterPro: IPR008774; Phospholip_A2.
DR Pfam: PF05826; Phospholip_A2; 1.
DR SMART: SM00085; PA2c; 1.

```

DR HSP; PF5445; 1A3D.  
DR FlyBase; FBN0029720; CG3009.  
DR GO; GO:000509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR InterPro; IPR008774; Phospholip\_A2.  
DR Pfam; PF05826; Phospholip\_A2; 1.  
DR SMART; SM00085; P2C2; 1.  
DR SMART; PS00118; P2 HUS; 1.  
DR PROSITE; PS00118; P2 HUS; 1.  
SQ SEQUENCE 342 AA; 38426 MW; 65E9A37ABEF4878 CRC64;

Query Match 8.1%; Score 86.5; DB 5; Length 281;  
Best Local Similarity 25.6%; Pred. No. 0.5;  
Matches 30; Conservative 15; Mismatches 49; Indels 23; Gaps 4;  
Matches 30; Conservative 15; Mismatches 49; Indels 23; Gaps 4;

QY 51 DSFLEILGGKNGVCQVRCRYGKAPMRPGYKQEPNGCGSYFLGLKVPESMDLGIAPM-T 109  
16 ESMVEL-----EEVCRQSGSYGHEFRGGLGIYPTGKWCGP---GTAATSYDDLGAHARE 68  
DB 110 KCNQLDVDCYDTGANKYR-----CDAKFRWCLXSTCSOLKRSGLGFV 151  
QY 110 KCNQLDVDCYDTGANKYR-----CDAKFRWCLXSTCSOLKRSGLGFV 151  
DB 69 RCRHEHMDCPDLNVNGECRGLNCRGTFRSHCHDCDARFRCICQAANTETANTLGA 125

RESULT 10  
Q9W410 PRELIMINARY; PRT; 342 AA.  
AC Q9W410  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CG3009 protein.  
GN CG3009.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celiniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glöckl A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RT Science 287:2185-2195 (2000).  
DR EMBL; AF003431; AAF45972.1; -.

DR HSP; PF5445; 1A3D.  
DR FlyBase; FBN0029720; CG3009.  
DR GO; GO:000509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR InterPro; IPR008774; Phospholip\_A2.  
DR Pfam; PF05826; Phospholip\_A2; 1.  
DR SMART; SM00085; P2C2; 1.  
DR SMART; PS00118; P2 HUS; 1.  
DR PROSITE; PS00118; P2 HUS; 1.  
SQ SEQUENCE 342 AA; 38426 MW; 65E9A37ABEF4878 CRC64;

Query Match 8.1%; Score 86.5; DB 5; Length 281;  
Best Local Similarity 25.6%; Pred. No. 0.5;  
Matches 30; Conservative 15; Mismatches 49; Indels 23; Gaps 4;  
Matches 30; Conservative 15; Mismatches 49; Indels 23; Gaps 4;

QY 51 DSFLEILGGKNGVCQVRCRYGKAPMRPGYKQEPNGCGSYFLGLKVPESMDLGIAPM-T 109  
16 ESMVEL-----EEVCRQSGSYGHEFRGGLGIYPTGKWCGP---GTAATSYDDLGAHARE 68  
DB 110 KCNQLDVDCYDTGANKYR-----CDAKFRWCLXSTCSOLKRSGLGFV 151  
QY 110 KCNQLDVDCYDTGANKYR-----CDAKFRWCLXSTCSOLKRSGLGFV 151  
DB 69 RCRHEHMDCPDLNVNGECRGLNCRGTFRSHCHDCDARFRCICQAANTETANTLGA 125

RESULT 10  
Q9W410 PRELIMINARY; PRT; 342 AA.  
AC Q9W410  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CG3009 protein.  
GN CG3009.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celiniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glöckl A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RT Science 287:2185-2195 (2000).  
DR EMBL; AF003431; AAF45972.1; -.

DR HSP; PF5445; 1A3D.  
DR FlyBase; FBN0029720; CG3009.  
DR GO; GO:000509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR InterPro; IPR008774; Phospholip\_A2.  
DR Pfam; PF05826; Phospholip\_A2; 1.  
DR SMART; SM00085; P2C2; 1.  
DR SMART; PS00118; P2 HUS; 1.  
DR PROSITE; PS00118; P2 HUS; 1.  
SQ SEQUENCE 342 AA; 38426 MW; 65E



```
Matches 30; Conservative 19; Mismatches 36; Indels 39; Gaps 6;
Qy 14 LGGGLAASDTSPTPE-----ESY-----SDWGLRLHRSFES-----VNSYFD 51
Db VGHNAALFDYTKGDSBELAQWNVYGTAAAGGIGYLTNDWAYHYFRGSMAGRINIGVYYTR 631
Qy 52 SFLEILGGKNGVCQVRCRYGKAMP-----RPGYKFPQPNCGSYFLGLK-----VPES 100
Db 632 GWQGVGTGDNGL-----WGRAALPNQAECPQGTGEGENKNCNGAIGDNNWHDLDPQG 685
Qy 101 MDLG 104
Db 686 REMG 689
RESULT 12
QBMQ50 PRELIMINARY; PRT; 117 AA.
AC QBMQ50;
DT 01-MAR-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2003 (TREMBlrel. 22, Last sequence update)
DE Hypothetical protein F44B9.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RT Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Fulton L.;
RT "The sequence of C. elegans cosmid F44B9.";
RT Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; L23648; AAM48524.1; -.
DR WormPep; F44B9.10; CE30988.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hypothetical protein.
SQ SEQUENCE 117 AA; 13359 MW; 51A3EB08F7BBE4C7 CRC64;
Query Match 7.9%; Score 84.5; DB 5; Length 117;
Best Local Similarity 25.2%; Pred. No. 0.28;
Matches 27; Conservative 13; Mismatches 48; Indels 19; Gaps 3;
Qy 63 VCQVRCRYGKAMPKPYK-----POEPNGCGSYFLGLKV-----PESMDLGIPTAMKCCNQ 114
Db 1 MCNVRCIYAVLFIVFLSKYIAQLVPEEFCGSGSISTSIYSTSSVFCQIQLNQCCMY 60
Qy 115 LDVCYDTCGANKYRCDAKFRWCLXSCDLKRSLGFSVKVEACDSLV 161
Db 61 HDLCYAGCTLPQMECDNQFCCELIATISN-----PFCQSIV 96
RESULT 13
QBMQ50 PRELIMINARY; PRT; 798 AA.
ID QBMQ50
AC Q96TF5 PRELIMINARY; PRT; 443 AA.
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mutant p53 binding protein 1 (MBP1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanka S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
```

```
QBMQ50;
AC Q96TF5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Integrin beta 1.
GN ITGB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK088729; BAC40532.1; -.
DR MGI; MGI:96610; Itgb1.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR003659; Plexin-like.
DR Pfam; PF00362; Integrin_B; 1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B; 1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS00243; INTEGRIN_BETA; 3.
SQ SEQUENCE 798 AA; 88246 MW; 8867DC4D55DBE898 CRC64;
Query Match 7.9%; Score 84; DB 11; Length 798;
Best Local Similarity 26.8%; Pred. No. 3.3;
Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;
Qy 26 DTEESYSDWGLRLHRSF-ESVNSYFDSFLEILGGKNGVCQVRCRYGKAMPKPYKPOE 84
Db 543 NTNEIYS-----GKFCEDNFNCDNSNGICGGNGVC--RCRVCE-----S80
Qy 85 PNGCGSYFLGLKVPEESMDLG--IPAMTKCCNOLDVCYDTCGANKYRC-DAKFRWCLXSLC 141
Db 581 ---CYPNVTGSAACDCSLDTGPGCLASNGQICNGRGIC--ECGACK--CTDPKQF--GPTC 630
Qy 142 SLDKRSLGFSVKVEACDSILVDTVTNTVTLGCRPPFNSORACICAEF 189
Db 631 ETCQTCGLGVCAEHKEC-----VQCRAF-NKGEKKTCAQE 664
RESULT 14
Q96TF5 PRELIMINARY; PRT; 443 AA.
ID Q96TF5
AC Q96TF5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mutant p53 binding protein 1 (MBP1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanka S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
```



```
RA Tanaka S., Sugimachi K., Sugimachi K.;
RT "Human mutant p53 binding protein (MBP1).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030655; BAA92880.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; F:blood coagulation; IEA.
DR InterPro; IPR001152; Asx hydroxylase.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF; 4.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00179; EGF CA; 4.
DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 443 AA; 49421 MW; 9CE175F4F388A56D CRC64;

Query Match 7.8%; Score 83.5; DB 4; Length 443;
Best Local Similarity 21.8%; Pred. No. 1.8;
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;

Qy 6 GFIVLV-----LSLGGGLAQSPTSPTESYSD---W---GLRHLR-----GSP 43
Db 10 GSLLLWALLLLLSASPDSEEDPSYTECHDGYEWDPSQCRDVECLTPEACKGEM 69

Qy 44 ESNVSYFDSFLELLGKNGVCQYRC-----RYGKAMP-----RPGYKP 82
Db 70 KCIHY-----GG-----YLCLPSAAVINDLHGEPPPPVPPAQHENPCPPGYEP 115

Qy 83 QEPNGCGSYFLGLKVPESMDLGIPTAMTKC-----CNQLDVCYDTGANKYR-----C--- 129
Db 116 DDQDSC-----VDVDECAQALHCRPSQDCHNLPFGSYQCTCPDGYRKIGPECYDI 165

Qy 130 -DAKFRWCLXSTCSPLKESL-----GF-----VSKVEACD---SLVDVTVENTVWTL 171
Db 166 DECRYRYCOHR-CVNLPFGSCRCQCPGFGQLPNNRSCVDVNECDMGAPCEQRCFNSYGTFF 224

Qy 172 GCR 174
Db 225 LCR 227

RESULT 15
Q87HH8 PRELIMINARY; PRT; 854 AA.
AC Q87HH8;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Nitrite reductase (NAD(P)H), large subunit.
GN VPA0987.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62330.1;
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001327; FAD_pyr_redox.
```

```
DR InterPro; IPR007419; Fer2 BFD.
DR InterPro; IPR006066; Nir Si.
DR InterPro; IPR006067; Nir_Sir_4Fe4S.
DR InterPro; IPR005117; Nir_sir_fer.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF04324; fer2_BFD; 1.
DR Pfam; PF01077; NIR_Sir; 1.
DR Pfam; PF03460; NIR_Sir_fer; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; ENDRDTASEI.
DR PRINTS; PR00397; SIROHAEM.
DR PROSITE; PS00365; NIR_Sir; 1.
KW Complete proteome.
SQ SEQUENCE 854 AA; 93571 MW; D0EC68D3CF42ABB6 CRC64;

Query Match 7.8%; Score 83.5; DB 16; Length 854;
Best Local Similarity 26.7%; Pred. No. 4.1;
Matches 32; Conservative 11; Mismatches 48; Indels 29; Gaps 5;

Qy 19 AQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGKNGVCQYRCRYGKAMPERP 78
Db 609 AQXDDLPETWRKLI DAG-----FETGQAYAKA---LRMAKTCVGSWTCRYG----- 651

Qy 79 GYKPPQEPNGCGSY-----FLGLKVPESMDLGIPTAMTKC-----NQLDVCYDTGANKYRC 129
Db 652 ---VQDSVGLGSYIENRYKGIPTPHKMKFGVSGCTRECAEAQKQKDLGIATDAGWNNMYC 708

Search completed: May 17, 2004, 10:43:44
Job time : 47 secs
```

Abg09375 Novel hum  
Abgi19489 Novel hum  
Abgi29035 T. gondi  
Aav25506 T. gondi  
Aay44335 Arabidops  
Aag15426 Arabidops  
Aag24858 Arabidops  
Aae35101 Arabidops  
Aae37930 Human Cgd  
Abg29088 Novel hum  
Aaw25770 Human hb5  
Aaw54075 Human tum  
Aay3626 Human D53  
Aay29624 Mouse D53  
Aay49953 Mouse D53  
Aba46333 Protein e  
Aba57054 Human pro  
Abu59376 Novel hum  
Aaw02376 Proteinase  
Aay20079 B. burgdo  
Aae15792 Xenopus l  
Aay20078 B. burgdo  
Aag32485 Arabidops  
Aao14856 Serratia  
Aao14857 Serratia  
Aae20980 Serratia  
Aae29089 Serratia  
Aay20109 B. burgdo  
Aag82956 NIT relat  
Abu38786 Protein e  
Aam68139 Photomab  
Aay77656 Human zin  
Aay20108 B. burgdo  
Aay00245 Enterococ  
Aap43464 E. faecal  
Aab88492 E. faecal  
Abu13743 Enterococ  
Aag54208 Arabidops  
Aag59322 Arabidops  
Aag08921 Arabidops  
Aag24650 Arabidops  
Aag36070 Arabidops  
Aag32484 Arabidops  
Aaw5070 Streptoco  
Aap54564 S. pneumo  
Aac45097 S. pneumo  
Aag08921 Arabidops  
Aag24520 Arabidops  
Aag46069 Arabidops  
Aag23454 Arabidops  
Aag32483 Arabidops  
Aab02394 S. pneumo  
Aab46234 Protein e  
Aay81569 Streptoco  
Aay91041 Alycia ca  
Aab78288 Amino aci  
Aag32653 Arabidops  
Aag46068 Arabidops  
Aab02394 S. pneumo  
Aay00135 Enterococ  
Aab43354 E. faecal  
Aab83392 Enterococ  
Aabul3633 Enterococ  
Aao16378 Murine pa  
Aay68739 Amino aci  
Aab96333 Putative  
Aay91036 Human car  
Aay91037 Rat carbo  
Aay91040 Murine ca  
Aam23880 Human EST  
Aag61920 Prostate  
Aab94326 Protein C  
Aab78283 Amino aci  
Aab78286 Amino aci  
Aab78287 Amino aci

26	7	3.6	171	4	ABG09337
27	7	3.6	172	4	ABG19489
28	7	3.6	176	4	ABY29035
29	7	3.6	176	4	AAU25506
30	7	3.6	191	3	AAU44335
31	7	3.6	191	3	AAU44335
32	7	3.6	191	3	AAU44335
33	7	3.6	191	3	AAU44335
34	7	3.6	191	3	AAU44335
35	7	3.6	191	3	AAU44335
36	7	3.6	204	2	AAU25770
37	7	3.6	204	2	AAU25770
38	7	3.6	204	2	AAU25770
39	7	3.6	204	2	AAU25770
40	7	3.6	204	2	AAU25770
41	7	3.6	204	2	AAU25770
42	7	3.6	204	2	AAU25770
43	7	3.6	204	2	AAU25770
44	7	3.6	204	2	AAU25770
45	7	3.6	204	2	AAU25770
46	7	3.6	204	2	AAU25770
47	7	3.6	204	2	AAU25770
48	7	3.6	204	2	AAU25770
49	7	3.6	204	2	AAU25770
50	7	3.6	204	2	AAU25770
51	7	3.6	204	2	AAU25770
52	7	3.6	204	2	AAU25770
53	7	3.6	204	2	AAU25770
54	7	3.6	204	2	AAU25770
55	7	3.6	204	2	AAU25770
56	7	3.6	204	2	AAU25770
57	7	3.6	204	2	AAU25770
58	7	3.6	204	2	AAU25770
59	7	3.6	204	2	AAU25770
60	7	3.6	204	2	AAU25770
61	7	3.6	204	2	AAU25770
62	7	3.6	204	2	AAU25770
63	7	3.6	204	2	AAU25770
64	7	3.6	204	2	AAU25770
65	7	3.6	204	2	AAU25770
66	7	3.6	204	2	AAU25770
67	7	3.6	204	2	AAU25770
68	7	3.6	204	2	AAU25770
69	7	3.6	204	2	AAU25770
70	7	3.6	204	2	AAU25770
71	7	3.6	204	2	AAU25770
72	7	3.6	204	2	AAU25770
73	7	3.6	204	2	AAU25770
74	7	3.6	204	2	AAU25770
75	7	3.6	204	2	AAU25770
76	7	3.6	204	2	AAU25770
77	7	3.6	204	2	AAU25770
78	7	3.6	204	2	AAU25770
79	7	3.6	204	2	AAU25770
80	7	3.6	204	2	AAU25770
81	7	3.6	204	2	AAU25770
82	7	3.6	204	2	AAU25770
83	7	3.6	204	2	AAU25770
84	7	3.6	204	2	AAU25770
85	7	3.6	204	2	AAU25770
86	7	3.6	204	2	AAU25770
87	7	3.6	204	2	AAU25770
88	7	3.6	204	2	AAU25770
89	7	3.6	204	2	AAU25770
90	7	3.6	204	2	AAU25770
91	7	3.6	204	2	AAU25770
92	7	3.6	204	2	AAU25770
93	7	3.6	204	2	AAU25770
94	7	3.6	204	2	AAU25770
95	7	3.6	204	2	AAU25770
96	7	3.6	204	2	AAU25770
97	7	3.6	204	2	AAU25770
98	7	3.6	204	2	AAU25770

```

ends
ts)
tell updates/sec

-----
AAREKEEL 194
-----
5107
-----
Description
Ada57403 Human sec
Ada41278 Human sec
Abol31978 Novel hum
Abol48024 Human sec
Aay27572 Human sec
Abp622920 Human pol
Ada56921 Human sec
Ada40769 Human sec
Aabr47739 Human sec
Ade08422 Novel pro
Abmc7608 Photorhab
Aau17876 Novel hum
Aar99965 Clah12 B-
Aar72674 Cladospor
Adb48041 Novel hum
Aar60689 M.kandler
Aau17876 Novel hum
Aab14126 Bordetell
Abg29089 Novel hum
Aar99961 Cladospor
Abr53058 Protein s
Aar72669 Cladospor
Aay29625 Human +5
Aay49952 Human +5
Aag42859 Arabidops
Aab14126 Bordetell

```

```

Core version 5.1.6
1993 - 2004 Comput
ing SW model
0:44:24 ; Search tim
(without
913.570
345
LGGGLAQ.....PFF
text 60.0
82547505 residues
chosen parameters:
00
1000 summaries
n04:*
08:*
08:*
08:*
1s:*
2s:*
3as:*
3Bs:*
4s:*
of results predicted
ual to the score of
s of the total sco
SUMMARIES
3 ID
5 ADA57403
5 ADA41278
5 ABO13378
5 ABR48024
2 AA271572
5 ABP62320
5 ADA56321
5 ADA40769
5 ABR47739
5 ABM67608
2 AAR99965
2 AAR72674
7 ADB48041
6 ABR60689
4 AAU17876
3 AAB14126
4 AEG39089
2 AAG99961
6 ABR53058
6 ABR72669
5 AAY29625
3 AA49952
3 AAG42859

```

OM protein - protein s	Copy
Run on: May 17	
Title: US-10-	
Perfect score: 194	
Sequence: 1 MOLA	
Scoring table: OLIGO	
Gapop	
Searched: 158610	
Word size : 0	
Total number of hits s	
Minimum DB seq length	
Maximum DB seq length	
Post-processing: List	
Database : A_Gen	
1: g	
2: g	
3: g	
4: g	
5: g	
6: g	
7: g	
8: g	
Pred. No. is the	
score greater th	
and is derived	
Result	Query
No.	Score Match
1	193 99.5
2	193 99.5
3	193 99.5
4	193 99.5
5	193 99.5
6	137 70.6
7	137 70.6
8	137 70.6
9	137 70.6
10	71 36.6
11	8 4.1
12	7 3.6
13	7 3.6
14	7 3.6
15	7 3.6
16	7 3.6
17	7 3.6
18	7 3.6
19	7 3.6
20	7 3.6
21	7 3.6
22	7 3.6
23	7 3.6
24	7 3.6

99	7	3.6	476	7	ADE83518	172	7	3.6	1217	7	ADD46290	113	7	ADD46290	Human Pro
100	7	3.6	476	7	ADD46264	173	7	3.6	1242	3	AAB53371	114	7	AAB53371	Human col
101	7	3.6	476	7	ADD46262	174	7	3.6	2515	4	ABB71354	115	7	ABB71354	Drosophil
102	7	3.6	491	3	AAB57137	175	6	3.1	6	2	RAW51565	116	6	RAW51565	Pre-seque
103	7	3.6	491	3	AAG73399	176	6	3.1	7	5	ABG77600	117	6	ABG77600	Targettin
104	7	3.6	491	4	AAE04143	177	6	3.1	9	5	ABB97041	118	6	ABB97041	Human tum
105	7	3.6	491	5	ABG64310	178	6	3.1	10	5	ABB97040	119	6	ABB97040	Human tum
106	7	3.6	491	5	ABG64288	179	6	3.1	14	4	AAW98665	120	6	AAW98665	Human pep
107	7	3.6	497	2	AAR60298	180	6	3.1	15	3	AAW87161	121	6	AAW87161	Human sec
108	7	3.6	502	4	AAW94448	181	6	3.1	15	4	AAE06138	122	6	AAE06138	Human gen
109	7	3.6	516	3	AAW59414	182	6	3.1	15	4	ABG67821	123	6	ABG67821	Human leu
110	7	3.6	516	3	AAW59414	183	6	3.1	15	5	ABG71130	124	6	ABG71130	SR protei
111	7	3.6	528	3	AAW57181	184	6	3.1	15	5	ABG33961	125	6	ABG33961	Human sec
112	7	3.6	528	3	AAW59413	185	6	3.1	16	3	AAW87162	126	6	AAW87162	Human sec
113	7	3.6	539	4	ABG29286	186	6	3.1	16	4	AAE06139	127	6	AAE06139	Human gen
114	7	3.6	540	3	AAW54206	187	6	3.1	16	5	ABG33962	128	6	ABG33962	Human sec
115	7	3.6	540	3	AAW54206	188	6	3.1	16	5	AAU97192	129	6	AAU97192	Human GPC
116	7	3.6	547	3	AAW59412	189	6	3.1	16	6	ABO06500	130	6	ABO06500	N-myristo
117	7	3.6	547	3	AAW59412	190	6	3.1	18	2	AAW71838	131	6	AAW71838	A.alterna
118	7	3.6	564	4	ABW58909	191	6	3.1	20	4	AAW20242	132	6	AAW20242	Peptide #
119	7	3.6	649	2	AAW70260	192	6	3.1	20	4	ABB40582	133	6	ABB40582	Peptide #
120	7	3.6	649	2	AAW70259	193	6	3.1	20	4	AAW34342	134	6	AAW34342	Peptide #
121	7	3.6	649	2	AAW70259	194	6	3.1	20	4	ABB24872	135	6	ABB24872	Protein #
122	7	3.6	650	2	AAW49107	195	6	3.1	20	4	AAW74230	136	6	AAW74230	Human bon
123	7	3.6	652	2	AAW63808	196	6	3.1	20	4	AAW61440	137	6	AAW61440	Human bra
124	7	3.6	652	2	AAW70499	197	6	3.1	20	4	ABG56032	138	6	ABG56032	Human liv
125	7	3.6	684	7	ADC37562	198	6	3.1	20	5	ABG44183	139	6	ABG44183	Human pep
126	7	3.6	722	5	ABG32998	199	6	3.1	22	2	ABG44183	140	6	ABG44183	Neuropept
127	7	3.6	759	2	AAW41927	200	6	3.1	22	2	AAW34039	141	6	AAW34039	Neuropept
128	7	3.6	759	2	AAW46593	201	6	3.1	25	4	ABG52659	142	6	ABG52659	Human liv
129	7	3.6	759	4	AAW92754	202	6	3.1	25	4	ABG40737	143	6	ABG40737	Human pep
130	7	3.6	771	7	ADC31519	203	6	3.1	29	4	ABW50870	144	6	ABW50870	Human sec
131	7	3.6	788	5	AAW47977	204	6	3.1	29	4	ABW50870	145	6	ABW50870	Human sec
132	7	3.6	791	6	ABO52988	205	6	3.1	29	4	AAO09139	146	6	AAO09139	Human pol
133	7	3.6	792	3	AAW42779	206	6	3.1	29	6	ABO45127	147	6	ABO45127	Novel hum
134	7	3.6	816	5	ABW33952	207	6	3.1	29	6	ABO45127	148	6	ABO45127	Novel hum
135	7	3.6	875	5	ABP62960	208	6	3.1	29	7	ABO26607	149	6	ABO26607	Protein a
136	7	3.6	894	5	ABP43352	209	6	3.1	29	7	ABO26874	150	6	ABO26874	Protein a
137	7	3.6	894	5	ABP43352	210	6	3.1	31	4	ABW40196	151	6	ABW40196	Peptide #
138	7	3.6	894	6	ABU13631	211	6	3.1	31	4	ABW40196	152	6	ABW40196	Peptide #
139	7	3.6	913	4	ABW62729	212	6	3.1	31	4	ABW40196	153	6	ABW40196	Peptide #
140	7	3.6	913	4	ABW62729	213	6	3.1	31	4	ABW40196	154	6	ABW40196	Peptide #
141	7	3.6	962	2	AAW00136	214	6	3.1	31	4	AAO09252	155	6	AAO09252	Human bon
142	7	3.6	962	2	AAW00132	215	6	3.1	31	4	AAW73660	156	6	AAW73660	Human bon
143	7	3.6	962	2	AAW00248	216	6	3.1	31	4	AAW60966	157	6	AAW60966	Human bra
144	7	3.6	962	2	AAW00248	217	6	3.1	31	4	ABG55395	158	6	ABG55395	Human liv
145	7	3.6	962	2	AAW00246	218	6	3.1	31	5	ABG43532	159	6	ABG43532	Human pep
146	7	3.6	962	2	AAW00134	219	6	3.1	32	5	ABW9043	160	6	ABW9043	Human imm
147	7	3.6	962	5	ABP43463	220	6	3.1	32	5	ABP29426	161	6	ABP29426	Streptoco
148	7	3.6	962	5	ABP43463	221	6	3.1	32	5	AAU97163	162	6	AAU97163	Human G-p
149	7	3.6	962	5	ABP43467	222	6	3.1	32	6	ABO06471	163	6	ABO06471	Human G-p
150	7	3.6	962	5	ABP43355	223	6	3.1	32	7	ABO33899	164	6	ABO33899	Anti-GPI-
151	7	3.6	962	5	ABP43353	224	6	3.1	33	2	AAW87260	165	6	AAW87260	KEKE-moti
152	7	3.6	962	5	ABP43353	225	6	3.1	33	2	AAW87260	166	6	AAW87260	KEKE-moti
153	7	3.6	962	5	ABP43351	226	6	3.1	34	4	ABW41266	167	6	ABW41266	Peptide #
154	7	3.6	962	6	ABU88491	227	6	3.1	34	4	ABW41266	168	6	ABW41266	Peptide #
155	7	3.6	962	6	ABU88379	228	6	3.1	34	4	AAW35051	169	6	AAW35051	Peptide #
156	7	3.6	962	6	ABU88383	229	6	3.1	34	4	ABW35051	170	6	ABW35051	Peptide #
157	7	3.6	962	6	ABU88439	230	6	3.1	34	4	ABW35051	171	6	ABW35051	Peptide #
158	7	3.6	962	6	ABU88495	231	6	3.1	34	4	ABW35051	172	6	ABW35051	Peptide #
159	7	3.6	962	6	ABU13634	232	6	3.1	34	4	ABW35051	173	6	ABW35051	Peptide #
160	7	3.6	962	6	ABU13746	233	6	3.1	39	4	AAW46689	174	6	AAW46689	Human imm
161	7	3.6	962	6	ABU13630	234	6	3.1	41	4	AAW15285	175	6	AAW15285	Peptide #
162	7	3.6	962	6	ABU13744	235	6	3.1	41	4	ABB29116	176	6	ABB29116	Peptide #
163	7	3.6	962	6	ABU13742	236	6	3.1	41	4	AAW67463	177	6	AAW67463	Human bon
164	7	3.6	962	6	ABU13632	237	6	3.1	41	4	AAW55070	178	6	AAW55070	Human bra
165	7	3.6	1083	6	ABW33704	238	6	3.1	44	4	AAW55070	179	6	AAW55070	Human rep
166	7	3.6	1137	4	ABW63815	239	6	3.1	44	4	AAW55070	180	6	AAW55070	Human rep
167	7	3.6	1131	7	ADDA6288	240	6	3.1	45	4	AAW91250	181	6	AAW91250	Human imm
168	7	3.6	1191	7	ADE63058	241	6	3.1	46	4	AAW91250	182	6	AAW91250	C Glutami
169	7	3.6	1203	7	ADP70304	242	6	3.1	46	4	AAW91250	183	6	AAW91250	C Glutami
170	7	3.6	1209	5	ABP73800	243	6	3.1	48	4	AAW91250	184	6	AAW91250	Drosophil
171	7	3.6	1211	4	ABB64663	244	6	3.1	48	4	AAW91250	185	6	AAW91250	Drosophil
												186	6	AAW91250	Human pol
												187	6	AAW91250	Human imm



391	6	3.1	78	6	ABR68196	Human sec	464	6	3.1	78	6	ABO27313	Human sec
392	6	3.1	78	6	ABU60588	Human sec	465	6	3.1	78	6	ABR68806	Human sec
393	6	3.1	78	6	ABU96249	Novel hum	466	6	3.1	78	6	ABO06622	Human sec
394	6	3.1	78	6	ABU92680	Human sec	467	6	3.1	78	6	ABR99167	Human sec
395	6	3.1	78	6	ABO08757	Human sec	468	6	3.1	78	6	ABU57051	Human PRO
396	6	3.1	78	6	ABO02809	Human sec	469	6	3.1	78	6	ABU86003	Novel hum
397	6	3.1	78	6	ABR74963	Human sec	470	6	3.1	78	6	ABU82290	Novel hum
398	6	3.1	78	6	ABR94725	Human sec	471	6	3.1	78	6	ABU87301	Human PRO
399	6	3.1	78	6	ABU13970	Human PRO	472	6	3.1	78	6	ABU83773	Human sec
400	6	3.1	78	6	ABU85698	Human PRO	473	6	3.1	78	6	ABO08147	Human PRO
401	6	3.1	78	6	ABU98858	Novel hum	474	6	3.1	78	6	ABU92508	Human sec
402	6	3.1	78	6	ABU98073	Novel hum	475	6	3.1	78	6	ABU1858	Novel hum
403	6	3.1	78	6	ABU91779	Novel hum	476	6	3.1	78	6	ABU66022	Novel hum
404	6	3.1	78	6	ABU89472	Human PRO	477	6	3.1	78	6	ABU81178	Human sec
405	6	3.1	78	6	ABU86313	Human sec	478	6	3.1	78	6	ABR59851	Human sec
406	6	3.1	78	6	ABU67526	Human sec	479	6	3.1	78	6	ABU94039	Novel hum
407	6	3.1	78	6	ABU080554	Human PRO	480	6	3.1	78	6	ABU99892	Novel hum
408	6	3.1	78	6	ABU72555	Novel hum	481	6	3.1	78	6	ABR6562	Human sec
409	6	3.1	78	6	ABU90908	Novel hum	482	6	3.1	78	6	ABR90980	Human sec
410	6	3.1	78	6	ABR99472	Human sec	483	6	3.1	78	6	ABO53293	Novel hum
411	6	3.1	78	6	ABR98862	Human sec	484	6	3.1	78	6	ABU59010	Human sec
412	6	3.1	78	6	ABO16385	Human sec	485	6	3.1	78	6	ABU94407	Human PRO
413	6	3.1	78	6	ABR92285	Human sec	486	6	3.1	78	6	ABU79289	Human PRO
414	6	3.1	78	6	ABO18926	Human sec	487	6	3.1	78	6	ABU86618	Human sec
415	6	3.1	78	6	ABU71984	Novel hum	488	6	3.1	78	6	ABU94712	Human PRO
416	6	3.1	78	6	ABU85083	Novel hum	489	6	3.1	78	6	ABO04639	Human PRO
417	6	3.1	78	6	ABU080222	Novel hum	490	6	3.1	78	6	ABR70388	Human sec
418	6	3.1	78	6	ABU08627	Novel hum	491	6	3.1	78	6	ABU92388	Novel hum
419	6	3.1	78	6	ABO08627	LS147-enc	492	6	3.1	78	6	ABU98553	Human PRO
420	6	3.1	78	6	ABO11554	Human sec	493	6	3.1	78	6	ABR65952	Human sec
421	6	3.1	78	6	ABO02199	Human sec	494	6	3.1	78	6	ABR64669	Human sec
422	6	3.1	78	6	ABU88773	Novel hum	495	6	3.1	78	6	ABU59453	Novel hum
423	6	3.1	78	6	ABU83468	Human sec	496	6	3.1	78	6	ABU79594	Human PRO
424	6	3.1	78	6	ABO06269	Novel hum	497	6	3.1	78	6	ABU92985	Human sec
425	6	3.1	78	6	ABR59305	Human sec	498	6	3.1	78	6	ABU95944	Human PRO
426	6	3.1	78	6	ABO09367	Human sec	499	6	3.1	78	6	ABU91164	Novel hum
427	6	3.1	78	6	ABO19231	Novel hum	500	6	3.1	78	6	ABU90257	Novel hum
428	6	3.1	78	6	ABO11249	Human sec	501	6	3.1	78	6	ABO09672	Human sec
429	6	3.1	78	6	ABR66867	Human sec	502	6	3.1	78	6	ABO10944	Human sec
430	6	3.1	78	6	ABO16080	Human sec	503	6	3.1	78	6	ABR70998	Human sec
431	6	3.1	78	6	ABO13786	Human sec	504	6	3.1	78	6	ABU98295	Novel hum
432	6	3.1	78	6	ABU71538	Human sec	505	6	3.1	78	6	ABU87606	Human PRO
433	6	3.1	78	6	ABU65689	Human sec	506	6	3.1	78	6	ABU93444	Human PRO
434	6	3.1	78	6	ABO07537	Human PRO	507	6	3.1	78	6	ABU89300	Novel hum
435	6	3.1	78	6	ABO03724	Human sec	508	6	3.1	78	6	ABU84688	Human sec
436	6	3.1	78	6	ABR67172	Human sec	509	6	3.1	78	6	ABR69778	Human sec
437	6	3.1	78	6	ABO15775	Human sec	510	6	3.1	78	6	ABU80155	Human PRO
438	6	3.1	78	6	ABU56056	Human sec	511	6	3.1	78	6	ABU82507	Novel hum
439	6	3.1	78	6	ABU72319	Human PRO	512	6	3.1	78	6	ABU92219	Novel hum
440	6	3.1	78	6	ABU65384	Human PRO	513	6	3.1	78	6	ABU93424	Human PRO
441	6	3.1	78	6	ABU95329	Novel hum	514	6	3.1	78	6	ABO09977	Human sec
442	6	3.1	78	6	ABU71232	Human PRO	515	6	3.1	78	6	ABO09062	Human sec
443	6	3.1	78	6	ABO07842	Human PRO	516	6	3.1	78	6	ABU96471	Human PRO
444	6	3.1	78	6	ABR70083	Human sec	517	6	3.1	78	6	ABU10925	Human PRO
445	6	3.1	78	6	ABR69416	Human sec	518	6	3.1	78	6	ABU10630	Human sec
446	6	3.1	78	6	ABO01557	Human PRO	519	6	3.1	78	6	ABU81677	Novel hum
447	6	3.1	78	6	ABU81359	Human PRO	520	6	3.1	78	6	ABU72141	Human PRO
448	6	3.1	78	6	ABR60156	Human sec	521	6	3.1	78	6	ABU95639	Human PRO
449	6	3.1	78	6	ABU90992	Human PRO	522	6	3.1	78	6	ABU96848	Novel hum
450	6	3.1	78	6	ABR67891	Human sec	523	6	3.1	78	6	ABR70693	Human sec
451	6	3.1	78	6	ABR65279	Human sec	524	6	3.1	78	6	ABO05044	Novel hum
452	6	3.1	78	6	ABR68501	Human sec	525	6	3.1	78	6	ABO08452	Human sec
453	6	3.1	78	6	ABR71913	Human sec	526	6	3.1	78	6	ABU88616	Human PRO
454	6	3.1	78	6	ABU59304	Human sec	527	6	3.1	78	6	ABO34130	Human PRO
455	6	3.1	78	6	ABU85393	Human PRO	528	6	3.1	78	6	ABO05659	Human sec
456	6	3.1	78	6	ABU89083	Human sec	529	6	3.1	78	6	ABO05659	Human sec
457	6	3.1	78	6	ABU83163	Human sec	530	6	3.1	78	6	ABR74048	Human sec
458	6	3.1	78	6	ABU95019	Novel hum	531	6	3.1	78	6	ABR95640	Human sec
459	6	3.1	78	6	ABU90567	Novel hum	532	6	3.1	78	6	ABR60937	Human sec
460	6	3.1	78	6	ABU84078	Human sec	533	6	3.1	78	6	ABR81242	Human sec
461	6	3.1	78	6	ABU93729	Novel hum	534	6	3.1	78	6	ABM00938	Human sec
462	6	3.1	78	6	ABO26001	Human PRO	535	6	3.1	78	6	ABR88540	Human sec
463	6	3.1	78	6	ABR64974	Human sec	536	6	3.1	78	6	ABM77361	Human sec

537	6	3.1	78	6	ABO28845	Human	sec	610	6	3.1	78	6	ABR87015	Human	sec
538	6	3.1	78	6	ABO31590	Human	sec	611	6	3.1	78	6	ABM11057	Human	sec
539	6	3.1	78	6	ABM08007	Human	sec	612	6	3.1	78	6	ABM28201	Human	sec
540	6	3.1	78	6	ABO40487	Human	sec	613	6	3.1	78	6	ABO32200	Human	sec
541	6	3.1	78	6	ABO35912	Human	PRO	614	6	3.1	78	6	ABM15327	Human	sec
542	6	3.1	78	6	ABO44051	Human	PRO	615	6	3.1	78	6	ABM06482	Human	sec
543	6	3.1	78	6	ADA77994	Human	sec	616	6	3.1	78	6	ABM04293	Human	sec
544	6	3.1	78	6	ABM24846	Human	sec	617	6	3.1	78	6	ABM22406	Human	sec
545	6	3.1	78	6	ABO03114	Human	sec	618	6	3.1	78	6	ABM07702	Human	sec
546	6	3.1	78	6	ABR90370	Human	sec	619	6	3.1	78	6	ABO40792	Human	sec
547	6	3.1	78	6	ABM17284	Human	sec	620	6	3.1	78	6	ABM35439	Human	sec
548	6	3.1	78	6	ABR95030	Human	sec	621	6	3.1	78	6	ABM33202	Human	sec
549	6	3.1	78	6	ABR95335	Human	sec	622	6	3.1	78	6	ABO50288	Human	sec
550	6	3.1	78	6	ADB17123	Human	tra	623	6	3.1	78	6	ABU99282	Human	sec
551	6	3.1	78	6	ABO21573	Human	sec	624	6	3.1	78	6	ABO04334	Human	sec
552	6	3.1	78	6	ABR97837	Human	sec	625	6	3.1	78	6	ABO05964	Human	sec
553	6	3.1	78	6	ABR787625	Human	sec	626	6	3.1	78	6	ABM18504	Human	sec
554	6	3.1	78	6	ABM77666	Human	sec	627	6	3.1	78	6	ADRA27999	Human	sec
555	6	3.1	78	6	ABM27896	Human	sec	628	6	3.1	78	6	ABR97532	Human	sec
556	6	3.1	78	6	ABM06177	Human	sec	629	6	3.1	78	6	ABR80632	Human	sec
557	6	3.1	78	6	ABM03683	Human	sec	630	6	3.1	78	6	ABR80632	Human	sec
558	6	3.1	78	6	ABM35134	Human	sec	631	6	3.1	78	6	ABM01243	Human	sec
559	6	3.1	78	6	ABM26371	Human	sec	632	6	3.1	78	6	ABR88845	Human	sec
560	6	3.1	78	6	ABO48153	Human	sec	633	6	3.1	78	6	ABM13497	Human	sec
561	6	3.1	78	6	ABR92895	Human	sec	634	6	3.1	78	6	ABM20881	Human	sec
562	6	3.1	78	6	ABO24656	Human	sec	635	6	3.1	78	6	ABO42012	Human	sec
563	6	3.1	78	6	ADA37874	Human	sec	636	6	3.1	78	6	ABO42622	Human	sec
564	6	3.1	78	6	ABM11667	Human	sec	637	6	3.1	78	6	ABO42622	Human	sec
565	6	3.1	78	6	ABM02768	Human	sec	638	6	3.1	78	6	ABM10142	Human	sec
566	6	3.1	78	6	ABM16064	Human	sec	639	6	3.1	78	6	ABO38657	Human	sec
567	6	3.1	78	6	ABO27625	Human	sec	640	6	3.1	78	6	ABM32897	Human	sec
568	6	3.1	78	6	ABM29116	Human	sec	641	6	3.1	78	6	ABM22711	Human	sec
569	6	3.1	78	6	ABM07092	Human	sec	642	6	3.1	78	6	ABM74922	Human	sec
570	6	3.1	78	6	ABM21186	Human	sec	643	6	3.1	78	6	ADA79786	Human	sec
571	6	3.1	78	6	ABM09532	Human	sec	644	6	3.1	78	6	ABR96312	Human	sec
572	6	3.1	78	6	ABO41402	Human	sec	645	6	3.1	78	6	ABM2463	Human	sec
573	6	3.1	78	6	ABO36217	Human	PRO	646	6	3.1	78	6	ABR86405	Human	sec
574	6	3.1	78	6	ABO43746	Human	PRO	647	6	3.1	78	6	ABR86710	Human	sec
575	6	3.1	78	6	ABM76446	Human	sec	648	6	3.1	78	6	ABM16674	Human	sec
576	6	3.1	78	6	ABM76142	Human	sec	649	6	3.1	78	6	ABM29726	Human	sec
577	6	3.1	78	6	ABM25761	Human	sec	650	6	3.1	78	6	ABO29150	Human	sec
578	6	3.1	78	6	ABM26066	Human	sec	651	6	3.1	78	6	ABM23321	Human	sec
579	6	3.1	78	6	ADA21560	Human	sec	652	6	3.1	78	6	ABM22101	Human	sec
580	6	3.1	78	6	ABO03419	Human	sec	653	6	3.1	78	6	ABO37742	Human	sec
581	6	3.1	78	6	ABO02504	Human	sec	654	6	3.1	78	6	ABM28506	Human	sec
582	6	3.1	78	6	ABO44271	Human	sec	655	6	3.1	78	6	ABM28811	Human	sec
583	6	3.1	78	6	ABR90675	Human	sec	656	6	3.1	78	6	ABM66455	Human	sec
584	6	3.1	78	6	ABR73743	Human	sec	657	6	3.1	78	6	ABM75837	Human	sec
585	6	3.1	78	6	ABO16995	Human	sec	658	6	3.1	78	6	ABM34117	Human	sec
586	6	3.1	78	6	ABR94420	Human	sec	659	6	3.1	78	6	ABM34422	Human	sec
587	6	3.1	78	6	ABR75927	Human	sec	660	6	3.1	78	6	ABO20353	Human	sec
588	6	3.1	78	6	ABR71303	Human	sec	661	6	3.1	78	6	ABO21268	Human	sec
589	6	3.1	78	6	ABR93200	Human	sec	662	6	3.1	78	6	ABO21268	Human	sec
590	6	3.1	78	6	ABR93505	Human	sec	663	6	3.1	78	6	ADA20100	Novel	hum
591	6	3.1	78	6	ADA10347	Human	sec	664	6	3.1	78	6	ABO34199	Human	sec
592	6	3.1	78	6	ABR87930	Human	sec	665	6	3.1	78	6	ABR96617	Human	sec
593	6	3.1	78	6	ABO27930	Human	sec	666	6	3.1	78	6	ADA94579	Human	sec
594	6	3.1	78	6	ABO30065	Human	sec	667	6	3.1	78	6	ABR85795	Human	sec
595	6	3.1	78	6	ABO33274	Human	PRO	668	6	3.1	78	6	ABR99777	Human	sec
596	6	3.1	78	6	ABM04962	Human	sec	669	6	3.1	78	6	ABM00328	Human	sec
597	6	3.1	78	6	ABM08922	Human	sec	670	6	3.1	78	6	ABM00633	Human	sec
598	6	3.1	78	6	ABO36522	Human	sec	671	6	3.1	78	6	ABO29760	Human	sec
599	6	3.1	78	6	ABO35607	Human	PRO	672	6	3.1	78	6	ABM23626	Human	sec
600	6	3.1	78	6	ABO39572	Human	sec	673	6	3.1	78	6	ABM29421	Human	sec
601	6	3.1	78	6	ABM10447	Human	sec	674	6	3.1	78	6	ABO38352	Human	sec
602	6	3.1	78	6	ABM11972	Human	PRO	675	6	3.1	78	6	ABO45652	Human	sec
603	6	3.1	78	6	ABO52118	Human	PRO	676	6	3.1	78	6	ABM20576	Human	sec
604	6	3.1	78	6	ABO52423	Human	PRO	677	6	3.1	78	6	ABM2576	Human	sec
605	6	3.1	78	6	ADA19928	Human	hum	678	6	3.1	78	6	ABM1690	Human	sec
606	6	3.1	78	6	ABO23741	Human	sec	679	6	3.1	78	6	ABO18316	Human	sec
607	6	3.1	78	6	ADB17311	Human	tra	680	6	3.1	78	6	ABO22743	Human	PRO
608	6	3.1	78	6	ADA17891	Human	PRO	681	6	3.1	78	6	ABO23048	Human	PRO
609	6	3.1	78	6	ABR97227	Human	sec	682	6	3.1	78	6	ABR92590	Human	sec

683	6	3.1	78	6	ABR81547	756	6	3.1	78	6	ADA00397	110	6	ADA00397	Human sec
684	6	3.1	78	6	ABR77971	757	6	3.1	78	6	ABM26981	111	6	ABM26981	Human sec
685	6	3.1	78	6	ABR89760	758	6	3.1	78	6	ABO03378	112	6	ABO03378	Human sec
686	6	3.1	78	6	ABM26676	759	6	3.1	78	6	ABO39877	113	6	ABO39877	Human sec
687	6	3.1	78	6	ABM13802	760	6	3.1	78	6	ABO49983	114	6	ABO49983	Human sec
688	6	3.1	78	6	ABO28540	761	6	3.1	78	6	ABO50898	115	6	ABO50898	Human sec
689	6	3.1	78	6	ABO30370	762	6	3.1	78	6	ABO53534	116	6	ABO53534	Human sec
690	6	3.1	78	6	ABM07397	763	6	3.1	78	6	ABR74658	117	6	ABR74658	Human sec
691	6	3.1	78	6	ABM03988	764	6	3.1	78	6	ABR77137	118	6	ABR77137	Human sec
692	6	3.1	78	6	ABO37132	765	6	3.1	78	6	ABM17894	119	6	ABM17894	Human sec
693	6	3.1	78	6	ABO41707	766	6	3.1	78	6	ABR95945	120	6	ABR95945	Human sec
694	6	3.1	78	6	ABO35302	767	6	3.1	78	6	ABO21878	121	6	ABO21878	Human sec
695	6	3.1	78	6	ABM25151	768	6	3.1	78	6	ABO20048	122	6	ABO20048	Human sec
696	6	3.1	78	6	ABO47543	769	6	3.1	78	6	ABO24351	123	6	ABO24351	Human sec
697	6	3.1	78	6	ABO47848	770	6	3.1	78	6	ABR86100	124	6	ABR86100	Human sec
698	6	3.1	78	6	ABO48458	771	6	3.1	78	6	ABM10752	125	6	ABM10752	Human sec
699	6	3.1	78	6	ABO51508	772	6	3.1	78	6	ABM76751	126	6	ABM76751	Human sec
700	6	3.1	78	6	ABO51813	773	6	3.1	78	6	ABR89455	127	6	ABR89455	Human sec
701	6	3.1	78	6	ABO50593	774	6	3.1	78	6	ABM12582	128	6	ABM12582	Human sec
702	6	3.1	78	6	ABR79717	775	6	3.1	78	6	ABO05872	129	6	ABO05872	Human sec
703	6	3.1	78	6	ABM16979	776	6	3.1	78	6	ABO34997	130	6	ABO34997	Human sec
704	6	3.1	78	6	ABO18011	777	6	3.1	78	6	ABM03073	131	6	ABM03073	Human sec
705	6	3.1	78	6	ABO20963	778	6	3.1	78	6	ABM19051	132	6	ABM19051	Human sec
706	6	3.1	78	6	ABR96922	779	6	3.1	78	6	ABM19356	133	6	ABM19356	Human sec
707	6	3.1	78	6	ADA38804	780	6	3.1	78	6	ABO46567	134	6	ABO46567	Human sec
708	6	3.1	78	6	ABM16369	781	6	3.1	78	6	ABO49068	135	6	ABO49068	Human sec
709	6	3.1	78	6	ABM24236	782	6	3.1	78	6	ABR69111	136	6	ABR69111	Human sec
710	6	3.1	78	6	ABM14717	783	6	3.1	78	6	ABR89150	137	6	ABR89150	Human sec
711	6	3.1	78	6	ABM04598	784	6	3.1	78	6	ABR72523	138	6	ABR72523	Human sec
712	6	3.1	78	6	ABM09227	785	6	3.1	78	6	ABR74353	139	6	ABR74353	Human sec
713	6	3.1	78	6	ABM06787	786	6	3.1	78	6	ABO18621	140	6	ABO18621	Human sec
714	6	3.1	78	6	ABO39267	787	6	3.1	78	6	ABR0327	141	6	ABR0327	Human sec
715	6	3.1	78	6	ABM75532	788	6	3.1	78	6	ABM01548	142	6	ABM01548	Human sec
716	6	3.1	78	6	ABM25456	789	6	3.1	78	6	ABM02158	143	6	ABM02158	Human sec
717	6	3.1	78	6	ABM19966	790	6	3.1	78	6	ABR87320	144	6	ABR87320	Human sec
718	6	3.1	78	6	ABO46872	791	6	3.1	78	6	ABM12887	145	6	ABM12887	Human sec
719	6	3.1	78	6	ABO47177	792	6	3.1	78	6	ABM30641	146	6	ABM30641	Human sec
720	6	3.1	78	6	ABO47177	793	6	3.1	78	6	ABM24541	147	6	ABM24541	Human sec
721	6	3.1	78	6	ADA83311	794	6	3.1	78	6	ABO29455	148	6	ABO29455	Human sec
722	6	3.1	78	6	ABR71608	795	6	3.1	78	6	ABO31285	149	6	ABO31285	Human sec
723	6	3.1	78	6	ABR72218	796	6	3.1	78	6	ABM14412	150	6	ABM14412	Human sec
724	6	3.1	78	6	ABR98557	797	6	3.1	78	6	ABM09837	151	6	ABM09837	Human sec
725	6	3.1	78	6	ABO06927	798	6	3.1	78	6	ABO38962	152	6	ABO38962	Human sec
726	6	3.1	78	6	ABR84880	799	6	3.1	78	6	ABM34727	153	6	ABM34727	Human sec
727	6	3.1	78	6	ABR73438	800	6	3.1	78	6	ABO51203	154	6	ABO51203	Human sec
728	6	3.1	78	6	ABR76532	801	6	3.1	78	6	ABO04029	155	6	ABO04029	Human sec
729	6	3.1	78	6	ABR73333	802	6	3.1	78	6	ABO10499	156	6	ABO10499	Human sec
730	6	3.1	78	6	ABM18199	803	6	3.1	78	6	ABO53216	157	6	ABO53216	Human sec
731	6	3.1	78	6	ABO20658	804	6	3.1	78	6	ABR7742	158	6	ABR7742	Human sec
732	6	3.1	78	6	ABO25401	805	6	3.1	78	6	ABR78952	159	6	ABR78952	Human sec
733	6	3.1	78	6	ABO25706	806	6	3.1	78	6	ABO24046	160	6	ABO24046	Human sec
734	6	3.1	78	6	ABR94115	807	6	3.1	78	6	ABR93810	161	6	ABR93810	Human sec
735	6	3.1	78	6	ADA92925	808	6	3.1	78	6	ABM01853	162	6	ABM01853	Human sec
736	6	3.1	78	6	ABR80022	809	6	3.1	78	6	ABM78276	163	6	ABM78276	Human sec
737	6	3.1	78	6	ABM11362	810	6	3.1	78	6	ABR90065	164	6	ABR90065	Human sec
738	6	3.1	78	6	ABO32969	811	6	3.1	78	6	ADA22486	165	6	ADA22486	Human sec
739	6	3.1	78	6	ABO30675	812	6	3.1	78	6	ABM27591	166	6	ABM27591	Human sec
740	6	3.1	78	6	ABO30980	813	6	3.1	78	6	ABM13192	167	6	ABM13192	Human sec
741	6	3.1	78	6	ABM27286	814	6	3.1	78	6	ABM14107	168	6	ABM14107	Human sec
742	6	3.1	78	6	ABM30031	815	6	3.1	78	6	ABM08312	169	6	ABM08312	Human sec
743	6	3.1	78	6	ABM05567	816	6	3.1	78	6	ABO40182	170	6	ABO40182	Human sec
744	6	3.1	78	6	ABM15632	817	6	3.1	78	6	ABO40182	171	6	ABO40182	Human sec
745	6	3.1	78	6	ABM08617	818	6	3.1	78	6	ABM74617	172	6	ABM74617	Human sec
746	6	3.1	78	6	ABO42317	819	6	3.1	78	6	ABM33812	173	6	ABM33812	Human sec
747	6	3.1	78	6	ABO38047	820	6	3.1	78	6	ABM20271	174	6	ABM20271	Human sec
748	6	3.1	78	6	ABO45957	821	6	3.1	78	6	ABO48763	175	6	ABO48763	Human sec
749	6	3.1	78	6	ABM66760	822	6	3.1	78	6	ABO22586	176	6	ABO22586	Human sec
750	6	3.1	78	6	ADB20354	823	6	3.1	78	6	ABR72828	177	6	ABR72828	Human sec
751	6	3.1	78	6	ABM19661	824	6	3.1	78	6	ABO15470	178	6	ABO15470	Human sec
752	6	3.1	78	6	ABO49373	825	6	3.1	78	6	ABR85185	179	6	ABR85185	Human sec
753	6	3.1	78	6	ABO49678	826	6	3.1	78	6	ABO15165	180	6	ABO15165	Human sec
754	6	3.1	78	6	ADA78606	827	6	3.1	78	6	ABO17300	181	6	ABO17300	Human sec
755	6	3.1	78	6	ABR88235	828	6	3.1	78	6	ABM17589	182	6	ABM17589	Human sec



829	6	3.1	78	7	ADA06652	Human sec	902	6	3.1	83	4	ABG28185	Novel hum
830	6	3.1	78	7	ADA39345	Human sec	903	6	3.1	84	5	ABP27263	Streptoco
831	6	3.1	78	7	ABR85490	Human sec	904	6	3.1	85	2	AAM69237	Mouse dec
832	6	3.1	78	7	ABM77056	Human sec	905	6	3.1	85	2	AAM19618	Peptide #
833	6	3.1	78	7	ABO28235	Human sec	906	6	3.1	85	4	ABB39272	Peptide #
834	6	3.1	78	7	ABM23016	Human sec	907	6	3.1	85	4	AAM32775	Peptide #
835	6	3.1	78	7	ABM30336	Human sec	908	6	3.1	85	4	ABB24101	Protein #
836	6	3.1	78	7	ABM21796	Human sec	909	6	3.1	85	4	AAM72531	Human bon
837	6	3.1	78	7	ABM21491	Human sec	910	6	3.1	85	4	AAO13783	Human pol
838	6	3.1	78	7	ABM15022	Human sec	911	6	3.1	85	4	AAM59936	Human bra
839	6	3.1	78	7	ABO41097	Human sec	912	6	3.1	85	4	ABG54222	Human liv
840	6	3.1	78	7	ABO36827	Human sec	913	6	3.1	85	5	ABG42351	Human pep
841	6	3.1	78	7	ABO37437	Human sec	914	6	3.1	86	4	AAB01370	Human gen
842	6	3.1	78	7	ABM75227	Human sec	915	6	3.1	86	4	ABB38901	Peptide #
843	6	3.1	78	7	ABM33507	Human sec	916	6	3.1	86	4	AAM32383	Peptide #
844	6	3.1	78	7	ABO46262	Human sec	917	6	3.1	86	4	ABB23894	Protein #
845	6	3.1	78	7	ADAB2677	Human sec	918	6	3.1	86	4	AAM72121	Human bon
846	6	3.1	78	7	ADB85639	Novel hum	919	6	3.1	86	4	AAM59552	Human bra
847	6	3.1	78	7	ADB96371	Human PRO	920	6	3.1	86	4	ABG53807	Human liv
848	6	3.1	78	7	ABM31861	Human sec	921	6	3.1	86	5	ABG41935	Human pep
849	6	3.1	78	7	ABM31251	Human sec	922	6	3.1	86	5	ABG64121	Human alb
850	6	3.1	78	7	ADB85985	Human sec	923	6	3.1	86	5	ABP34623	Human ORF
851	6	3.1	78	7	ABM32166	Human sec	924	6	3.1	87	4	ABB41455	Peptide #
852	6	3.1	78	7	ABM32471	Human sec	925	6	3.1	87	4	ABB39647	Peptide #
853	6	3.1	78	7	ADB68318	Human PRO	926	6	3.1	87	4	AAM33219	Peptide #
854	6	3.1	78	7	ADB68125	Human PRO	927	6	3.1	87	4	ABB24327	Protein #
855	6	3.1	78	7	ABM31556	Human sec	928	6	3.1	87	4	AAM75130	Human bon
856	6	3.1	78	7	ABM30946	Human sec	929	6	3.1	87	4	AAM72995	Human bon
857	6	3.1	78	7	ADB90942	Novel hum	930	6	3.1	87	4	AAM60359	Human bra
858	6	3.1	78	7	ADCS57843	Human PRO	931	6	3.1	87	4	AAM62329	Human bra
859	6	3.1	78	7	ADCS5207	Human PRO	932	6	3.1	87	4	ABG54706	Human liv
860	6	3.1	78	7	ADC12074	Human sec	933	6	3.1	87	4	ABG56893	Human liv
861	6	3.1	78	7	ADC07022	Human PRO	934	6	3.1	87	5	ABG42834	Human pep
862	6	3.1	78	7	ADCS6496	Human PRO	935	6	3.1	87	5	ABG44807	Human pep
863	6	3.1	78	7	ADC17201	Mammalian	936	6	3.1	89	4	AAM73176	Human bon
864	6	3.1	78	7	ADC07551	Human sec	937	6	3.1	89	4	AAM60521	Human bra
865	6	3.1	78	7	ADC11541	Human sec	938	6	3.1	89	4	ABG54893	Human liv
866	6	3.1	78	7	ADC14899	Novel hum	939	6	3.1	89	4	AU20122	Human DNA
867	6	3.1	78	7	ADCS2394	Novel hum	940	6	3.1	89	5	ABG43023	Human pep
868	6	3.1	78	7	ADC14663	Novel hum	941	6	3.1	89	5	ABG91371	Novel hum
869	6	3.1	78	7	ADD08195	Novel hum	942	6	3.1	90	4	AAO02084	Human pol
870	6	3.1	78	7	ADC82020	Human PRO	943	6	3.1	90	4	AAU41384	Propionib
871	6	3.1	78	7	ADD07662	Novel hum	944	6	3.1	90	6	ABM37903	Protein e
872	6	3.1	78	7	ADC82553	Human PRO	945	6	3.1	91	2	AAU27150	EST clone
873	6	3.1	78	7	ADP05715	Human sec	946	6	3.1	91	2	AAU96704	Peptide #
874	6	3.1	78	7	ADP08733	Novel hum	947	6	3.1	91	3	AAO36640	Human sec
875	6	3.1	78	7	ADP06982	Novel hum	948	6	3.1	91	4	AAM14470	Peptide #
876	6	3.1	78	7	ADC83229	Human PRO	949	6	3.1	91	4	ABM33418	Peptide #
877	6	3.1	78	7	ADP55336	Human PRO	950	6	3.1	91	4	ABM26883	Peptide #
878	6	3.1	78	7	ADP36070	Novel hum	951	6	3.1	91	4	ABE28243	Human pep
879	6	3.1	78	7	ADP56294	Human PRO	952	6	3.1	91	4	ABB18877	Protein #
880	6	3.1	78	7	ADP54732	Human PRO	953	6	3.1	91	4	AAM66597	Human bon
881	6	3.1	78	7	ADE26886	Novel hum	954	6	3.1	91	4	AAM54203	Human bra
882	6	3.1	78	7	ADE26353	Novel hum	955	6	3.1	91	4	ABG48265	Human liv
883	6	3.1	78	8	ADCS2204	Novel hum	956	6	3.1	91	4	AAM02197	Peptide #
884	6	3.1	78	8	ADE74379	Human sec	957	6	3.1	91	5	ABG36249	Human pep
885	6	3.1	78	8	ADE74991	Human sec	958	6	3.1	91	7	ABO22464	Mosquito
886	6	3.1	79	3	ABG19780	Arabidops	959	6	3.1	91	7	ABO22464	Mosquito
887	6	3.1	79	6	ADA21097	Human sec	960	6	3.1	91	7	ADP587032	Human pan
888	6	3.1	79	6	ADC94077	E. faeciu	961	6	3.1	92	5	AAM48271	Human org
889	6	3.1	80	4	AAM15956	Peptide #	962	6	3.1	92	5	AAU83176	Novel sec
890	6	3.1	80	4	ABB34951	Peptide #	963	6	3.1	92	5	AAU83176	Novel sec
891	6	3.1	80	4	AAM28459	Peptide #	964	6	3.1	93	7	ADC31534	Human nov
892	6	3.1	80	4	ABB29773	Peptide #	965	6	3.1	94	2	AAU31902	Soybean c
893	6	3.1	80	4	ABE20361	Human bon	966	6	3.1	95	3	AAU31902	Soybean c
894	6	3.1	80	4	AAM68137	Human bra	967	6	3.1	96	4	AAO09002	Arabidops
895	6	3.1	80	4	AAM55755	Human bra	968	6	3.1	97	3	AAU09002	Arabidops
896	6	3.1	80	4	ABG49782	Human liv	969	6	3.1	97	3	ABP41625	Breast an
897	6	3.1	80	4	AAM03694	Peptide #	970	6	3.1	98	4	ABM58896	Breast an
898	6	3.1	80	4	ABG23746	Novel hum	971	6	3.1	98	4	ABP41625	Human ova
899	6	3.1	80	5	ABG37662	Human pep	972	6	3.1	98	4	ABM406077	Caenorhab
900	6	3.1	82	4	ABM61106	Human her	973	6	3.1	98	4	ABM406077	Caenorhab
901	6	3.1	82	4	AAB84791	E8 death	974	6	3.1	98	4	ABM406077	Caenorhab



975 6 3.1 98 5 ABP10105  
976 6 3.1 98 5 ABG44514  
977 6 3.1 99 4 AAM18386  
978 6 3.1 99 4 AAM17289  
979 6 3.1 99 4 ABB36294  
980 6 3.1 99 4 ABB37417  
981 6 3.1 99 4 AAM29789  
982 6 3.1 99 4 AAM30865  
983 6 3.1 99 4 ABB31098  
984 6 3.1 99 4 ABB32171  
985 6 3.1 99 4 ABB22715  
986 6 3.1 99 4 AAM70545  
987 6 3.1 99 4 AAM57065  
988 6 3.1 99 4 AAM58098  
989 6 3.1 99 4 ABB51129  
990 6 3.1 99 4 ABB52224  
991 6 3.1 99 4 AAM05983  
992 6 3.1 99 5 ABG39076  
993 6 3.1 99 5 ABG40200  
994 6 3.1 100 4 ABB11267  
995 6 3.1 101 4 ABB11285  
996 6 3.1 102 7 ADD12477  
997 6 3.1 103 4 AAU41738  
998 6 3.1 103 5 ABP03545  
999 6 3.1 103 6 ABB38257  
1000 6 3.1 106 5 AAE20908

# ALIGNMENTS

RESULT 1  
ADA57403  
ID ADA57403 standard; protein; 194 AA.

XX AC ADA57403;  
XX AC  
XX DT 20-NOV-2003 (first entry)  
XX DE Human secreted protein #204.  
XX KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytosolic; cerebroprotective; neuroprotective; nootropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.  
XX OS Homo sapiens.  
XX PN WO2002102994-A2.  
XX PD 27-DEC-2002.  
XX PF 19-MAR-2002; 2002WO-US008278.  
XX PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Rosen CA, Ruben SM;  
XX PI WPI; 2003-167512/16.  
DR N-PSDB; ADA56510.  
XX New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or

PT neurodegenerative disorders.  
XX Claim 13; SEQ ID NO 1596; 1754pp; English.  
PS The invention relates to 592 new human secreted polypeptides useful for  
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 95% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC of antisense DNA or RNA, in gene therapy, for identifying individuals  
CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for  
CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence data for  
CC this patent did form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 194 AA;

Query Match 99.5%; Score 193; DB 6; Length 194;  
Best Local Similarity 100.0%; Pred. No. 3.7e-186;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLASGLVWLISLGGGLAOSDTSPTDEESVSDMGLRHLSGFSVNSYFDSFLELLGGK 60  
DB 1 MKLASGLVWLISLGGGLAOSDTSPTDEESVSDMGLRHLSGFSVNSYFDSFLELLGGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQPFNGCGSYFLGLKVPESMDLGIPTAMTKCNOLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKQPFNGCGSYFLGLKVPESMDLGIPTAMTKCNOLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXSLCSDLKRSIGFVSKVEACDSLVDTVTNTWTLCGRPFMNSQ 180  
DB 121 TCGANKYRCDAKFRWCLXSLCSDLKRSIGFVSKVEACDSLVDTVTNTWTLCGRPFMNSQ 180  
QY 181 RAACICAEKEEKEEL 194  
DB 181 RAACICAEKEEKEEL 194

RESULT 2  
ADA41278  
ID ADA41278 standard; protein; 194 AA.  
XX ADA41278;  
XX AC  
XX DT 20-NOV-2003 (first entry)  
XX DE Human secreted protein.  
XX KW Human; secreted protein; cancer; hyperproliferative disorder;  
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;  
KW anaemia; allergic reaction; asthma; cardiovascular disorder;  
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;  
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;  
KW vulnery; cardiant; gene therapy.

XX Homo sapiens.  
XX WO3002102993-A2.  
XX 27-DEC-2002.  
XX 19-MAR-2002; 2002WO-US008123.  
XX 21-MAR-2001; 2001US-0277340P.  
XX 19-JUL-2001; 2001US-0306171P.  
XX 13-NOV-2001; 2001US-0331287P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM;  
XX WPI; 2003-175238/17.  
XX New human secreted proteins and nucleic acid molecules, useful for  
XX preparing a diagnostic or pharmaceutical composition for diagnosing,  
XX preventing or treating cancer or other hyperproliferative disorder,  
XX asthma, allergies or AIDS.  
XX Claim 1; SEQ ID NO 1561; 3205pp; English.  
XX The invention relates to novel genes ADA39629-ADA40565 and proteins  
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,  
XX treating or ameliorating medical conditions e.g. by protein or gene  
XX therapy. The polypeptides, nucleic acid molecules, antibodies or their  
XX fragments, and agonists or antagonists that bind to the polypeptide are  
XX useful for preparing a diagnostic or pharmaceutical composition for  
XX diagnosing or treating cancer or other hyperproliferative disorder. The  
XX polypeptides and nucleic acid molecules are also useful for detecting,  
XX preventing, diagnosing, prognosticating, treating or ameliorating cancer  
XX or other hyperproliferative disorders including neoplasms, autoimmune  
XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus  
XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic  
XX anaemia), haematopoietic or haematological disorders (e.g. anaemia,  
XX thrombocytopenia), allergic reactions including asthma or eczema,  
XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory  
XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.  
XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders  
XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,  
XX fungal or viral infections including HIV/AIDS), or wound healing and  
XX disorders of epithelial cell proliferation. The nucleic acids are also  
XX useful for chromosome identification, radiation hybrid mapping or long-  
XX range restriction mapping, as molecular weight markers, or as  
XX hybridization or diagnostic probes. The polypeptides and antibodies are  
XX useful for providing immunological probes for differential identification  
XX of the tissues immunohistochemistry assays. Note: The sequence data for  
XX this patent did not form part of the printed specification, but was  
XX obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 194 AA;  
Query Match 99.5%; Score 193; DB 6; Length 194;  
Best Local Similarity 100.0%; Pred. No. 3.7e-186;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLASGLFVLWLSGGGLAQSDDTSPDEESVSDWGLRHLRGSPESVNSYFDSFLEILGGK 60  
DB 1 MKLASGLFVLWLSGGGLAQSDDTSPDEESVSDWGLRHLRGSPESVNSYFDSFLEILGGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQPFNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKQPFNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120  
QY 121 TCGANKYRCDAKFWCLXKSICSDLKRLSIGFVSKVEACDSLVDVTFTNTWTLGCRPFMNSQ 180  
DB 121 TCGANKYRCDAKFWCLXKSICSDLKRLSIGFVSKVEACDSLVDVTFTNTWTLGCRPFMNSQ 180

QY 181 RAACICAEKEEKEEL 194  
DB 181 RAACICAEKEEKEEL 194  
RESULT 3  
ABO13978  
ID ABO13978 standard; protein; 194 AA.  
XX ABO13978;  
XX 21-AUG-2003 (first entry)  
XX Novel human secreted protein #7.  
XX Human; secreted protein; cytostatic; neuroprotective; hepatotropic;  
XX gene therapy; cancer; liver disorder; hepatitis; neural disorder;  
XX Alzheimer's disease.  
XX Homo sapiens.  
XX US2003028003-A1.  
XX 06-FEB-2003.  
XX 12-OCT-2001; 2001US-00974879.  
XX 07-NOV-1997; 97US-0064900P.  
XX 07-NOV-1997; 97US-0064908P.  
XX 07-NOV-1997; 97US-0064911P.  
XX 07-NOV-1997; 97US-0064912P.  
XX 07-NOV-1997; 97US-0064983P.  
XX 07-NOV-1997; 97US-0064984P.  
XX 07-NOV-1997; 97US-0064985P.  
XX 07-NOV-1997; 97US-0064987P.  
XX 07-NOV-1997; 97US-0064988P.  
XX 07-NOV-1997; 97US-0066089P.  
XX 17-NOV-1997; 97US-0066090P.  
XX 17-NOV-1997; 97US-0066094P.  
XX 17-NOV-1997; 97US-0066095P.  
XX 17-NOV-1997; 97US-0066100P.  
XX 04-NOV-1998; 98WO-US023435.  
XX 05-MAY-1999; 99US-00305736.  
XX 13-OCT-2000; 2000US-0239893P.  
XX 28-MAR-2001; 2001US-00818683.  
XX (ROSE/) ROSEN C A.  
XX (FENG/) FENG P.  
XX (RUBE/) RUBEN S M.  
XX (EBNE/) EBNER R.  
XX (OLSE/) OLSEN H S.  
XX (NIJ/) NI J.  
XX (WEI/) WEI Y.  
XX (SOPE/) SOPPET D R.  
XX (MOOR/) MOORE P A.  
XX (KIAY/) KYAW H.  
XX (LAFL/) LAFLEUR D W.  
XX (SHIV/) SHI Y.  
XX (JANA/) JANAT F.  
XX (ENDR/) ENDRESS G A.  
XX (CART/) CARTER K C.  
XX (BIRS/) BIRSE C E.  
XX Rosen CA, Feng P, Ruben SM, Ebner R, Olsen HS, Ni J, Wei Y;  
XX Soppet DR, Moore PA, Kyaw H, Lafleur DW, Shi Y, Janat F;  
XX Endress GA, Carter KC, Birse CE;  
XX WPI; 2003-479549/45.  
XX N-PSDB; ACD18865.  
XX New nucleic acid molecule, useful for preparing a medicament for  
XX preventing, treating or ameliorating a medical condition e.g., cancer,  
XX liver disorders such as hepatitis or neural disorders such as Alzheimer's

PT disease.  
XX  
PS Claim 11; Page 357; 496pp; English.  
XX  
CC The invention describes a new isolated nucleic acid molecule comprising a  
CC sequence having at least 95% identity with a sequence comprising: (a) a  
CC polynucleotide (PN) fragment of a sequence comprising 420-3435 bp, or its  
CC allelic variant; (b) a PN fragment of the cDNA sequence; (c) a PN  
CC sequence encoding a polypeptide, or its fragment, domain, epitope or  
CC species homologue; or (d) a PN that hybridises under stringent conditions  
CC to any one of the sequences of (A)-(C). The nucleic acid is useful for  
CC preparing a medicament for preventing, treating or ameliorating a medical  
CC condition e.g., cancer, liver disorders such as hepatitis or neural  
CC disorders such as Alzheimer's disease. This is the amino acid sequence of  
CC a novel human secreted protein  
XX  
XX Sequence 194 AA;

Query Match 99.5%; Score 193; DB 6; Length 194;  
Best Local Similarity 100.0%; Pred. No. 3.7e-186;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLASGFLVLSLGGGLAQSPTSPTDEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
DB 1 MKLASGFLVLSLGGGLAQSPTSPTDEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKPPQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKPPQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXSI CSDLKRSILGFVSKVEACDSLVDVTWNTVTLGCRPFMNSQ 180  
DB 121 TCGANKYRCDAKFRWCLXSI CSDLKRSILGFVSKVEACDSLVDVTWNTVTLGCRPFMNSQ 180  
QY 181 RAACICAEKEEEL 194  
DB 181 RAACICAEKEEEL 194

RESULT 4  
ID ABR48024  
XX ABR48024 standard; protein; 194 AA.  
AC ABR48024;  
XX  
DT 12-JUN-2003 (first entry)  
DE Human secreted protein, SEQ ID 915.  
XX  
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;  
KW vulnery; antiinflammatory; nootropic; neuroprotective;  
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.  
XX  
OS Homo sapiens.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PF 19-MAR-2002; 2002WO-US009785.  
XX 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA Rosen CA, Ruben SW;  
XX  
PI WPI; 2003-129429/12.  
DR  
XX Novel human secreted proteins, useful for detecting, preventing,  
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular

PT disorders such as arrhythmia.  
XX  
PS Claim 13; SEQ ID NO 915; 1881pp; English.  
XX  
CC The present invention relates to novel human secreted proteins (ABR47633-  
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins  
CC and their coding sequences are useful for the preparation of a diagnostic  
CC or pharmaceutical composition for diagnosing or treating a cardiovascular  
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary  
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune  
CC system disorders, muscular disorders, reproductive disorders,  
CC gastrointestinal disorders, pulmonary disorders, renal disorders, for  
CC proliferative disorders and/or cancerous diseases and conditions, for  
CC wound healing and epithelial cell proliferation, to treat inflammation or  
CC infection, for treating thrombosis and arteriosclerosis, for treating or  
CC preventing neural damage which occurs in neurological disorders or  
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
CC disease, to enhance bone and periodontal regeneration and aid in tissue  
CC transplants or bone grafts, to prevent skin aging or hair loss, to  
CC stimulate growth and differentiation of haematopoietic cells and bone  
CC marrow cells when used in combination with other cytokines, to maintain  
CC organs before transplantation or for supporting cell culture of primary  
CC tissues, to increase or decrease differentiation or proliferation of  
CC embryonic stem cells, or to modulate mammalian characteristics or  
CC metabolism. Note: The sequence data for this patent was published in  
CC electronic format and is available from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 194 AA;

Query Match 99.5%; Score 193; DB 6; Length 194;  
Best Local Similarity 100.0%; Pred. No. 3.7e-186;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLASGFLVLSLGGGLAQSPTSPTDEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
DB 1 MKLASGFLVLSLGGGLAQSPTSPTDEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKPPQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKPPQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXSI CSDLKRSILGFVSKVEACDSLVDVTWNTVTLGCRPFMNSQ 180  
DB 121 TCGANKYRCDAKFRWCLXSI CSDLKRSILGFVSKVEACDSLVDVTWNTVTLGCRPFMNSQ 180  
QY 181 RAACICAEKEEEL 194  
DB 181 RAACICAEKEEEL 194

RESULT 5  
ID AAY27572  
XX AAY27572 standard; protein; 195 AA.  
AC AAY27572;  
XX  
DT 30-JUL-1999 (first entry)  
DE Human secreted protein encoded by gene No. 6.  
XX  
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX  
OS Homo sapiens.  
XX  
XX WO9924836-A1.  
PN

XX 20-MAY-1999.  
 XX 04-NOV-1998; 98WO-US023435.  
 XX 07-NOV-1997; 97US-0064900P.  
 XX 07-NOV-1997; 97US-0064908P.  
 XX 07-NOV-1997; 97US-0064911P.  
 XX 07-NOV-1997; 97US-0064912P.  
 XX 07-NOV-1997; 97US-0064983P.  
 XX 07-NOV-1997; 97US-0064984P.  
 XX 07-NOV-1997; 97US-0064985P.  
 XX 07-NOV-1997; 97US-0064987P.  
 XX 07-NOV-1997; 97US-0064988P.  
 XX 07-NOV-1997; 97US-0066089P.  
 XX 17-NOV-1997; 97US-0066090P.  
 XX 17-NOV-1997; 97US-0066094P.  
 XX 17-NOV-1997; 97US-0066095P.  
 XX 17-NOV-1997; 97US-0066100P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Feng P, Carter KC, Endress GA, Rosen CA, Ruben SM, Janat F;  
 XX Ni J, Wei Y, Moore PA, Soppet DR, Kyaw H, Lafleur DW, Olsen HS;  
 XX Shi Y, Ebner R;  
 XX WPI; 1999-337740/28.  
 XX N-PSDB; AAX84938.  
 XX New human secreted proteins and coding sequences useful for treating  
 XX disorders of the immune system and hyperproliferative disorders.  
 XX Claim 11; Page 352-353; 507pp; English.  
 XX This sequence represents a secreted human protein encoded by the gene  
 XX clone detailed in the descriptor line. The gene can be used to generate  
 XX fusion proteins by linking to the gene to a human immunoglobulin Fc  
 XX portion (e.g. AAX84924) for increasing the stability of the fused protein  
 XX as compared to the human protein only. The invention relates to 125 novel  
 XX genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino  
 XX acid sequences AAY27567-Y27933) which are useful for preventing, treating  
 XX or ameliorating medical conditions e.g. by protein or gene therapy. Also,  
 XX pathological conditions can be diagnosed by determining the amount of the  
 XX new polypeptides in a sample or by determining the presence of mutations  
 XX in the new polynucleotides. Specific uses are described for each of the  
 XX 125 polynucleotides, based on which tissues they are most highly  
 XX expressed in (see AAX84933 for described uses)  
 XX Sequence 195 AA;  
 XX  
 XX Query Match 99.5%; Score 193; DB 2; Length 195;  
 XX Best Local Similarity 100.0%; Pred. No. 3.7e-186;  
 XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
 Db 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
 QY 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 Db 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 QY 121 TCGANKYRCDAKFRWCL 137  
 Db 121 TCGANKYRCDAKFRWCL 137  
 QY 181 RAACICAEKEEL 194  
 Db 181 RAACICAEKEEL 194

ID ABP62920 standard; protein; 194 AA.  
 XX AC ABP62920;  
 XX DT 14-OCT-2002 (first entry)  
 XX Human polypeptide SEQ ID NO 357.  
 XX Human; vulnery; dermatological; neuroprotective; nootropic; cancer;  
 XX antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;  
 XX antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;  
 XX burn; central nervous system disorder; Alzheimer's disease;  
 XX Parkinson's disease; Huntington's disease; immune disorder;  
 XX autoimmune disorder; multiple sclerosis; diabetes; allergy.  
 XX Homo sapiens.  
 XX WO200218424-A2.  
 XX 07-MAR-2002.  
 XX 31-AUG-2001; 2001WO-US027093.  
 XX 01-SEP-2000; 2000US-00654935.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Raundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
 XX Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;  
 XX WPI; 2002-583321/62.  
 XX N-PSDB; ABQ93399.  
 XX New polynucleotide and polypeptides, useful for treatment and diagnosis  
 XX of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral  
 XX sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple  
 XX sclerosis, diabetes and allergies.  
 XX Claim 20; SEQ ID NO 357; 284pp + Sequence Listing; English.  
 XX The invention relates to an isolated polynucleotide (I) comprising one of  
 XX 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising  
 XX administering to a mammalian subject a composition comprising the protein  
 XX (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).  
 XX (I), (II) and (III) are useful for diagnostic evaluation of disorders.  
 XX (I) is useful for gene therapy of diseases and (II) can be used for  
 XX therapeutic treatment. Diseases that may be treated include wound healing  
 XX and tissue repair, burns, central nervous system disorders (e.g.  
 XX Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral  
 XX sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple  
 XX sclerosis, diabetes and allergies. Note: The sequence data for this  
 XX patent did not form part of the printed specification, but was obtained  
 XX in electronic format directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 194 AA;  
 XX  
 XX Query Match 70.6%; Score 137; DB 5; Length 194;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-129;  
 XX Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
 Db 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFVSNSYFDSFLELLGGK 60  
 QY 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 Db 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
 QY 121 TCGANKYRCDAKFRWCL 137  
 Db 121 TCGANKYRCDAKFRWCL 137

RESULT 7  
ADA56921  
ADA56921 standard; protein; 194 AA.  
ADA56921;  
20-NOV-2003 (first entry)  
Human secreted protein #204.  
immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
cystostatic; cerebroprotective; neuroprotective; nootropic;  
cardiovascular; antiarteriosclerotic; gene therapy;  
human secreted protein; immune disorder; inflammation;  
respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
triple helix formation; antisense gene therapy; forensic biology.  
Homo sapiens.  
WC02002102994-A2.  
27-DEC-2002.  
19-MAR-2002; 2002WO-US008278.  
21-MAR-2001; 2001US-0277340P.  
19-JUL-2001; 2001US-0306171P.  
13-NOV-2001; 2001US-0331287P.  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Ruben SM;  
WPI; 2003-167512/16.  
N-PSDB; ADA56025.  
New human secreted polypeptides and polynucleotides, useful for  
diagnosing, treating or preventing e.g. immune disorders, inflammatory  
conditions, respiratory disorders, cancers, CNS disorders, or  
neurodegenerative disorders.  
Claim 13; SEQ ID NO 1111; 1754pp; English.  
The invention relates to 592 new human secreted polypeptides useful for  
diagnosing, treating or preventing e.g. immune disorders, inflammatory  
conditions, respiratory disorders, cancers, CNS disorders, or  
neurodegenerative disorders, or polypeptides comprising an amino acid  
sequence at least 95% identical to the new sequences. The polypeptides,  
antibodies or antibody fragments that bind to the polypeptides, nucleic  
acids encoding the polypeptides, agonists or antagonists that binds to  
the polypeptide, are useful in preparing diagnostic or pharmaceutical  
compositions for diagnosing, treating or preventing an e.g. immune  
disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
(e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
polynucleotides are useful for chromosome identification, chromosome  
mapping, for controlling gene expression through triple helix formation  
or antisense DNA or RNA, in gene therapy, for identifying individuals  
from minute biological samples, in forensic biology, and as hybridization  
probes. The polypeptides are useful for as molecular weight markers on  
sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
gels, to raise antibodies, for testing biological activities, and for  
treating or preventing neural disorders, immune system disorders,  
muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
renal, proliferative and/or cancerous diseases. This sequence corresponds  
to the polypeptide of the invention. Note: The sequence data for

diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.

Claim 13; SEQ ID NO 630; 1881bp; English.

The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue disease, to enhance bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: the sequence data for this patent was published in electronic format and is available from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 194 AA;

Query Match 70.6%; Score 137; DB 6; Length 194;

Best Local Similarity 100.0%; Pred. No. 1.1e-129; Indels 0; Gaps 0;

Matches 137; Conservative 0; Mismatches 0;

QY 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLSFESVNSYFDSFLELLGGK 60

DB 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120

DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120

QY 121 TCGANKYRCDAKFRWCL 137

DB 121 TCGANKYRCDAKFRWCL 137

RESULT 10

ADE08422

ID ADE08422 standard; protein; 335 AA.

XX ADE08422;

XX 29-JAN-2004 (first entry)

DT Novel protein (useful for identifying genetic disorders) #577.

DE novel gene; novel protein; tissue marker; molecular weight marker;

KW chromosome marker; genetic disorder.

XX Unidentified.

XX WO2003054152-A2.

PN 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 14-MAR-2002; 2002US-0365384P.

preventing, diagnosing, prognosticating, treating or ameliorating cancer or other hyperproliferative disorders including neoplasms, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematological disorders (e.g. anaemia, thrombocytopenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory bowel disease or Crohn's disease), neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial, fungal or viral infections including HIV/AIDS), or wound healing and disorders of epithelial cell proliferation. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping, as molecular weight markers, or as hybridization or diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 194 AA;

Query Match 70.6%; Score 137; DB 6; Length 194;

Best Local Similarity 100.0%; Pred. No. 1.1e-129;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLSFESVNSYFDSFLELLGGK 60

DB 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120

DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120

QY 121 TCGANKYRCDAKFRWCL 137

DB 121 TCGANKYRCDAKFRWCL 137

RESULT 9

ABR47739

ID ABR47739 standard; protein; 194 AA.

XX ABR47739;

XX 12-JUN-2003 (first entry)

DE Human secreted protein, SEQ ID 630.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;

KW vulnary; antiinflammatory; nootropic; neuroprotective;

KW antiparkinsonian; gene therapy; human; cardiovascular disorder.

XX Homo sapiens.

XX WO200295010-A2.

XX 28-NOV-2002.

XX 19-MAR-2002; 2002WO-US009785.

XX 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing,

Mon May 17 11:51:01 2004

PR 12-APR-2002; 2002US-0372381P.  
 PR 12-APR-2002; 2002US-0372615P.  
 PR 22-APR-2002; 2002US-00128558.  
 PR 24-APR-2002; 2002US-0376045P.  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Tang YT, Auandi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
 XX WPI; 2003-569235/53.  
 DR N-PSDB; ADE07511.  
 XX  
 XX New polynucleotides, useful for expressing recombinant proteins for  
 PT analysis, characterization or therapeutic use, or as markers for tissues  
 PT in which the corresponding protein is preferentially expressed.  
 XX  
 XX Claim 20; SEQ ID NO 1488; 1177pp; English.  
 PS  
 XX The invention comprises the amino acid and coding sequences of novel  
 CC proteins. The DNA and protein sequences of the invention are useful as:  
 CC markers for tissues in which the corresponding protein is preferentially  
 CC expressed; as molecular weight markers on gels; as chromosome markers or  
 CC tags; to identify chromosomes or to map related gene positions; and to  
 CC compare with endogenous DNA sequences in patients to identify potential  
 CC genetic disorders. The present amino acid sequence represents a protein  
 CC of the invention.  
 XX  
 XX Sequence 335 AA;  
 SQ  
 Query Match 36.6%; Score 71; DB 7; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-63; Indels 0; Gaps 0;  
 Matches 71; Conservative 0; Mismatches 0;  
 Qy 1 MKLASGFLVLMISLGGGLAQSDTSPDTEESYSDWGLRHRLGSFVSNSYFDSFLELLGGK 60  
 Db 1 MKLASGFLVLMISLGGGLAQSDTSPDTEESYSDWGLRHRLGSFVSNSYFDSFLELLGGK 60  
 Qy 61 NGVCQYRCRYG 71  
 Db 61 NGVCQYRCRYG 71  
 RESULT 11  
 ABM67608  
 ID ABM67608 standard; protein; 439 AA.  
 AC ABM67608;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 DE Photorhabdus luminescens protein sequence #705.  
 XX  
 XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
 KW detection; food; gene expression; plant; animal; microorganism; toxin;  
 KW antibiotic; biopesticide; virulence factor; disease model; plague;  
 KW whooping cough.  
 XX  
 XX Photorhabdus luminescens.  
 OS  
 XX WO200294867-A2.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX 07-FEB-2002; 2002WO-IB003040.  
 PF  
 XX 07-FEB-2001; 2001FR-00001659.  
 PR (INSP ) INST PASTEUR.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 PA  
 XX Duclaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
 PI

PI Buchrieser C;  
 XX WPI; 2003-148459/14.  
 XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
 XX  
 XX Claim 2; SEQ ID NO 705; 1205pp; French.  
 PS  
 XX The invention relates to the isolation of genes and their encoded  
 CC proteins from Photorhabdus luminescens. The isolated sequences are  
 CC sources of probes and primers for detecting the genome of P. luminescens  
 CC and related species; to study polymorphisms; for gene analysis and for  
 CC detection/amplification of the genes. Antibodies (Ab) raised against the  
 CC polypeptides encoded by the genes are used for detection/identification  
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
 CC carry a gene-containing vector are used to select compounds that  
 CC modulate, regulate, induce or inhibit expression of the genes in plants,  
 CC animals or microorganisms other than P. luminescens and are able to alter  
 CC response or sensitivity to toxins and antibiotics produced by P.  
 CC luminescens. Cells transformed to express the genes are useful for  
 CC recombinant production of the proteins, particularly toxins and  
 CC antibacterials useful as insecticides, bactericides and fungicides. The  
 CC genes, proteins, vectors containing the genes and Ab are also useful  
 CC therapeutically (to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.  
 CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens proteins  
 XX  
 XX Sequence 439 AA;  
 SQ  
 Query Match 4.1%; Score 8; DB 6; Length 439;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 SLGGGLAQ 20  
 Db 343 SLGGGLAQ 350  
 RESULT 12  
 AAR99965  
 ID AAR99965 standard; protein; 19 AA.  
 XX  
 XX AAR99965;  
 XX  
 XX 16-OCT-2003 (revised)  
 DT 21-MAY-1997 (first entry)  
 DE  
 DE Clah12 B-cell epitope (residues 87-105).  
 XX  
 XX Clah12; Clah 8; Cladosporium herbarum allergen; diagnosis; therapy;  
 KW stimulate; proliferation; interleukin production; T cell; tolerance.  
 XX  
 XX Davidiella tassiana.  
 OS  
 XX WO9627005-A2.  
 PN  
 XX 06-SEP-1996.  
 PD  
 XX 01-MAR-1996; 96WO-AT000038.  
 PF  
 XX 02-MAR-1995; 95AT-00000379.  
 PR (BIOM-) BIOMAY PROD & HANDELS GMBH.  
 PA  
 XX Achatz G, Oberkofler H, Simon B, Unger A, Lechenauer E, Kraft D;  
 PI Breitenbach M;  
 XX WPI; 1996-412772/41.  
 DR  
 XX



Mon May 17 11:51:01 2004

DNA encoding allergens of Cladosporium herbarum - useful for diagnosis and treatment of allergy.

Claim 7; Page 11; 20pp; German.

AAR99963-65 are B-cell epitopes of Cladosporium herbarum allergen, Clah12 (AAR99961). Clah12 and ifg fragments are useful in diagnosis and therapy, esp. in vitro detection of allergy to Clah8/12 by reactivity with serum IgE or cellular reaction to these allergens. Therapeutically they may stimulate proliferation and interleukin prod. in T cells, in vitro or in vivo, and also block T cells (induce tolerance of allergen-specific T cells). The use of allergen-deriv. but non-anaphylactic peptides allows larger doses to be admin. improving hypersensitisation therapy. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 19 AA;

Query Match 3.6%; Score 7; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193  
DB 7 ABEKEE 13  
|||||

RESULT 13  
ID AAR72674 standard; peptide; 23 AA.  
XX AAR72674;  
AC AAR72674;  
XX 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 25-OCT-1995 (first entry)  
XX Cladosporium herbarum allergen Clah11 B-cell epitope (85-107).  
XX Fungal spore; allergen; Clah11; allergy; ribosomal protein; RLA2;  
KW B-cell epitope; antigenic region.  
XX Davidiella tassiana.  
OS WO9506121-A2.  
XX 02-MAR-1995.  
PD 24-AUG-1994; 94WO-AT000120.  
PF 27-AUG-1993; 93AT-00001725.  
XX (BIOM-) BIOMAY PROD & HANDELSGES MBH.  
XX Achatz G, Oberkofler H, Simon B, Unger A, Lechenauer E;  
PI Hirschwehr R, Ebner C, Kraft D, Prillinger H, Breitenbach M;  
XX WPI; 1995-106850/14.  
DR Allergens derived from Cladosporium herbarum spores - also recombinant DNA for expressing the allergens, useful for in vitro allergy detection.  
XX Claim 1; Page 27; 35pp; German.  
XX Spores of Cladosporium herbarum are the most common fungal spores found in the air; they can cause allergic reactions. Various Clah allergens and sequences encoding them have now been isolated. The mature Clah11 allergen has mol. wt. 11 kD and is encoded by cDNA sequence AAQ87846. The allergen has homology to the ribosomal protein RLA2. Potential epitopic subfragments were identified by computer analysis of the amino acid sequence. See AAR72670-R72674 for potential B-cell epitopes and AAR72675-R72677 for potential T-cell epitopes. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

SQ Sequence 23 AA;

Query Match 3.6%; Score 7; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193  
DB 10 ABEKEE 16  
|||||

RESULT 14  
ID ADB48041 standard; protein; 34 AA.  
XX ADB48041;  
AC ADB48041;  
XX 04-DEC-2003 (first entry)  
DT Novel human secreted protein associated polypeptide #120.  
DE human; secreted protein; insulin; haemoglobin S; haemoglobin B;  
KW superoxide; SOD; catalase; DNA repair protein; oncogene;  
KW tumour suppressor; tumour necrosis factor; TNF; inflammation;  
KW blood vessel growth inhibition; immune response; immune system disorder;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW peripheral artery disease; limb ischaemia; arterio-arterial fistula;  
KW arteriovenous fistula; congenital heart defect;  
KW neovascularisation disorder; wound healing;  
KW epithelial cell proliferation; neurological disease; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; mania; dementia;  
KW infectious disease.  
XX Homo sapiens.  
OS US2003054443-A1.  
PN 20-MAR-2003.  
XX 04-OCT-2001; 2001US-00969730.  
PF 05-AUG-1997; 97US-0054798P.  
XX 05-AUG-1997; 97US-0054803P.  
PR 05-AUG-1997; 97US-0054804P.  
PR 05-AUG-1997; 97US-0054806P.  
PR 05-AUG-1997; 97US-0054807P.  
PR 05-AUG-1997; 97US-0054808P.  
PR 05-AUG-1997; 97US-0054809P.  
PR 05-AUG-1997; 97US-0055309P.  
PR 05-AUG-1997; 97US-0055310P.  
PR 05-AUG-1997; 97US-0055311P.  
PR 05-AUG-1997; 97US-0055312P.  
PR 18-AUG-1997; 97US-0055970P.  
PR 18-AUG-1997; 97US-0055986P.  
PR 19-AUG-1997; 97US-0056364P.  
PR 19-AUG-1997; 97US-0056365P.  
PR 19-AUG-1997; 97US-0056366P.  
PR 19-AUG-1997; 97US-0056367P.  
PR 19-AUG-1997; 97US-0056370P.  
PR 19-AUG-1997; 97US-0056371P.  
PR 19-AUG-1997; 97US-0056557P.  
PR 19-AUG-1997; 97US-0056563P.  
PR 19-AUG-1997; 97US-0056731P.  
PR 19-AUG-1997; 97US-0056732P.  
PR 04-AUG-1998; 98WO-US016235.  
PR 04-FEB-1999; 99US-00244112.  
PR 06-OCT-2000; 2000US-0238291P.  
PR 01-FEB-2001; 2001US-00774639.  
XX (RUBE/) RUBEN S M.  
PA (SOPP/) SOPPET D R.  
PA (EBNE/) EBNER R.



25-MAR-2003 (revised)  
 26-JUN-1995 (first entry)  
 M.kandleri topoisomerase V proteolytic fragment.  
 TI; supercoiled DNA; relaxing; closed circular DNA; sequencing; cloning;  
 amplification; probe.  
 Methanopyrus kandleri.  
 WO9421811-A1.  
 29-SEP-1994.  
 24-MAR-1994; 94WO-US003217.  
 24-MAR-1993; 93US-00038343.  
 (SLES/) SLESAREV A I.  
 Slesarev AI;  
 WPI; 1994-317030/39.  
 New thermostable DNA topoisomerase - obtd. from Methanopyrus kandleri,  
 used for relaxing supercoiled DNA and unlinking closed circular DNA.  
 Claim 10; Page 70; 104pp; English.  
 The sequence is that of a proteolytic fragment of a new topoisomerase  
 (TI) from Methanopyrus kandleri. The TI is a type I-group B TI whose  
 reaction proceeds via a transient single stranded break which changes the  
 linking number in steps of one and operates on duplex DNA. The TI can be  
 used for relaxing supercoiled DNA or for unlinking closed circular DNA.  
 See also AAR60684-90. (Updated on 25-MAR-2003 to correct PN field.)

DT 25-MAR-2003 (revised)  
 DT 26-JUN-1995 (first entry)  
 XX M.kandleri topoisomerase V proteolytic fragment.  
 DE TI; supercoiled DNA; relaxing; closed circular DNA; sequencing; cloning;  
 XX amplification; probe.  
 KW Methanopyrus kandleri.  
 KW OS  
 XX WO9421811-A1.  
 XX 29-SEP-1994.  
 XX 24-MAR-1994; 94WO-US003217.  
 XX 24-MAR-1993; 93US-00038343.  
 XX (SLES/) SLESAREV A I.  
 XX Slesarev AI;  
 XX WPI; 1994-317030/39.  
 XX New thermostable DNA topoisomerase - obtd. from Methanopyrus kandleri,  
 XX used for relaxing supercoiled DNA and unlinking closed circular DNA.  
 XX Claim 10; Page 70; 104pp; English.  
 XX The sequence is that of a proteolytic fragment of a new topoisomerase  
 XX (TI) from Methanopyrus kandleri. The TI is a type I-group B TI whose  
 XX reaction proceeds via a transient single stranded break which changes the  
 XX linking number in steps of one and operates on duplex DNA. The TI can be  
 XX used for relaxing supercoiled DNA or for unlinking closed circular DNA.  
 XX See also AAR60684-90. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 35 AA;  
 Query Match 3.6%; Score 7; DB 2; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194  
 Db 10 EEEKEEL 16  
 Search completed: May 17, 2004, 10:51:41  
 Job time : 111 secs

(OLSE/) OLSEN H S.  
 (YOUN/) YOUNG P E.  
 (GREE/) GREENE J M.  
 (FERR/) FERRIE A M.  
 (YUGG/) YU G.  
 (NIJ/) NI J.  
 (ROSE/) ROSEN C A.  
 (BREM/) BREWER L A.  
 (JANA/) JANAT F.  
 (BIRSE/) BIRSE C E.  
 Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM;  
 Ferrie AM, Yu G, Ni J, Rosen CA, Brewer LA, Janat F, Birse CE;  
 WPI; 2003-695903/66.  
 Novel human secreted proteins useful for treating and/or diagnosing  
 disorders of immune system, cardiovascular disorders such as peripheral  
 artery disease, neurological diseases such as Alzheimer's disease.  
 Disclosure; Page 54; 333pp; English.

The invention relates to novel human secreted proteins. The protein is  
 useful for preventing, treating or ameliorating a medical condition. The  
 protein is useful for diagnosing a pathological condition or  
 susceptibility to a pathological condition in a subject. The protein is  
 useful for identifying a binding partner. The nucleic acid is useful for  
 diagnosing pathological condition or a susceptibility to pathological  
 condition in a subject. The protein is useful as reagents for  
 differential identification of the tissues or cell types present in a  
 biological sample. The protein can be administered to patients having  
 absent or decreased levels of polypeptides e.g. insulin, to supplement  
 absent or decreased levels of different polypeptides, e.g. haemoglobin S  
 for haemoglobin B, superoxide (SOD), catalase, DNA repair protein, to  
 inhibit the activity of a polypeptide e.g. an oncogene or tumour  
 suppressor, to activate the activity of polypeptide e.g. by binding to a  
 receptor, to reduce the activity of membrane bound receptor by competing  
 with it for free ligand e.g. soluble tumour necrosis factor (TNF)  
 receptors used in reducing inflammation, or to bring about a desired  
 response e.g. blood vessel growth inhibition, enhancement of immune  
 acid are useful for treating, preventing, detecting, diagnosing disorders  
 of immune system involving abnormal growth of specific types of cells as  
 well as of other cell types where expression has been observed. The  
 protein, the nucleic acid and antibodies are useful for treating,  
 preventing and/or diagnosing diseases, disorders and/or conditions of  
 immune system, hyperproliferative disorders including neoplasms,  
 cardiovascular disorders (such as peripheral artery disease, limb  
 ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital  
 heart defects, etc), neovascularisation disorders, wound healing and  
 epithelial cell proliferation, neurological diseases (such as Alzheimer's  
 disease, Parkinson's disease, Huntington's disease, mania, dementia,  
 etc), infectious diseases caused by virus, bacteria, fungi, etc. The  
 present sequence represents the amino acid sequence of a novel human  
 secreted protein associated polypeptide.

Sequence 34 AA;  
 Query Match 3.6%; Score 7; DB 7; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LMLSLGG 16  
 Db 2 LMLSLGG 8

RESULT 15  
 AAR60689  
 ID AAR60689 standard; protein; 35 AA.  
 XX  
 AC AAR60689;  
 XX

Mon May 17 11:51:01 2004

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:49:45 ; Search time 23 Seconds  
(without alignments)  
435.454 Million cell updates/sec

Title: US-10-621-401-145  
Perfect score: 194  
Sequence: 1 MKLASGLVWLWLSGGGLAQ.....PFMNSORACICAEKEEL 194

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	4.1	214	1	US-08-155-171B-16
2	8	4.1	214	2	US-08-435-998-16
3	7	3.6	35	1	US-08-038-343A-5
4	7	3.6	106	1	US-08-185-414E-4
5	7	3.6	144	4	US-09-250-609-2
6	7	3.6	144	4	US-09-250-611-2
7	7	3.6	176	4	US-09-216-393B-73
8	7	3.6	191	4	US-09-134-000C-3705
9	7	3.6	204	2	US-08-715-204-1
10	7	3.6	204	2	US-08-691-814B-10
11	7	3.6	204	3	US-09-162-597-1
12	7	3.6	204	4	US-09-250-609-4
13	7	3.6	204	4	US-09-250-609-9
14	7	3.6	204	4	US-09-250-611-4
15	7	3.6	204	4	US-09-250-611-9
16	7	3.6	264	4	US-09-540-936-2978
17	7	3.6	320	4	US-09-818-739-6
18	7	3.6	320	4	US-09-818-739-7
19	7	3.6	320	4	US-09-071-035-472
20	7	3.6	388	4	US-09-252-991A-27381
21	7	3.6	396	3	US-08-961-083-16
22	7	3.6	396	4	US-09-536-784-16
23	7	3.6	434	3	US-08-111-939-13
24	7	3.6	434	3	US-09-233-989-7
25	7	3.6	435	1	US-08-111-939-14
26	7	3.6	435	1	US-08-111-939-15
27	7	3.6	435	1	US-08-111-939-16

28	7	3.6	435	1	US-08-452-262-2	Sequence 2, Appli
29	7	3.6	435	1	US-08-734-550-2	Sequence 2, Appli
30	7	3.6	435	5	PCT-US96-07528-2	Sequence 2, Appli
31	7	3.6	454	4	US-09-071-035-252	Sequence 252, App
32	7	3.6	476	3	US-09-233-989-2	Sequence 2, Appli
33	7	3.6	476	3	US-09-233-989-3	Sequence 3, Appli
34	7	3.6	476	3	US-09-233-989-6	Sequence 6, Appli
35	7	3.6	497	1	US-08-295-670-6	Sequence 6, Appli
36	7	3.6	497	1	US-08-633-485-6	Sequence 6, Appli
37	7	3.6	649	3	US-08-800-291B-5	Sequence 6, Appli
38	7	3.6	649	3	US-08-800-291B-6	Sequence 4, Appli
39	7	3.6	650	3	US-08-800-291B-4	Sequence 2, Appli
40	7	3.6	652	1	US-08-050-684-2	Sequence 1, Appli
41	7	3.6	652	1	US-08-582-719-2	Sequence 1, Appli
42	7	3.6	759	1	US-08-676-967-1	Sequence 1, Appli
43	7	3.6	759	1	US-08-676-974-1	Sequence 1, Appli
44	7	3.6	759	2	US-09-098-487-1	Sequence 1, Appli
45	7	3.6	894	4	US-09-071-035-248	Sequence 248, App
46	7	3.6	962	4	US-09-071-035-246	Sequence 246, App
47	7	3.6	962	4	US-09-071-035-250	Sequence 250, App
48	7	3.6	962	4	US-09-071-035-254	Sequence 254, App
49	7	3.6	962	4	US-09-071-035-470	Sequence 470, App
50	7	3.6	962	4	US-09-071-035-478	Sequence 478, App
51	7	3.6	962	4	US-09-071-035-478	Sequence 478, App
52	7	3.6	970	4	US-09-134-000C-5691	Sequence 5691, App
53	7	3.6	1245	4	US-09-252-991A-30935	Sequence 30935, A
54	6	3.1	9	4	US-09-285-630-7	Sequence 7, Appli
55	6	3.1	15	4	US-09-482-273-200	Sequence 200, App
56	6	3.1	16	4	US-09-482-273-201	Sequence 201, App
57	6	3.1	29	4	US-09-205-258-823	Sequence 823, App
58	6	3.1	29	4	US-09-205-258-1090	Sequence 1090, Ap
59	6	3.1	64	4	US-09-621-976-5995	Sequence 5995, Ap
60	6	3.1	71	4	US-08-311-731A-388	Sequence 388, App
61	6	3.1	71	4	US-09-543-681A-7079	Sequence 7079, Ap
62	6	3.1	75	4	US-09-621-976-7639	Sequence 7639, Ap
63	6	3.1	75	4	US-09-621-976-7640	Sequence 7640, Ap
64	6	3.1	77	4	US-09-621-976-6046	Sequence 6046, Ap
65	6	3.1	79	4	US-09-107-532A-3704	Sequence 3704, Ap
66	6	3.1	80	4	US-09-621-976-6829	Sequence 6829, Ap
67	6	3.1	82	3	US-09-382-155-6	Sequence 6, Appli
68	6	3.1	82	3	US-09-074-044A-6	Sequence 6, Appli
69	6	3.1	85	3	US-08-772-440-32	Sequence 32, Appli
70	6	3.1	87	4	US-09-489-847-326	Sequence 326, App
71	6	3.1	91	4	US-09-345-236B-132	Sequence 132, App
72	6	3.1	96	4	US-09-134-000C-5832	Sequence 5832, Ap
73	6	3.1	98	3	US-08-857-076-58	Sequence 58, Appli
74	6	3.1	105	4	US-09-621-976-4565	Sequence 4565, Ap
75	6	3.1	111	1	US-08-185-414E-2	Sequence 2, Appli
76	6	3.1	113	4	US-09-732-210-420	Sequence 420, App
77	6	3.1	114	4	US-09-621-976-5145	Sequence 5145, Ap
78	6	3.1	116	1	US-08-478-039-103	Sequence 103, App
79	6	3.1	116	1	US-08-476-349A-103	Sequence 103, App
80	6	3.1	119	4	US-09-621-976-5148	Sequence 5148, Ap
81	6	3.1	123	4	US-09-482-273-175	Sequence 175, App
82	6	3.1	124	4	US-09-252-991A-22831	Sequence 22831, A
83	6	3.1	127	4	US-09-173-300-40	Sequence 40, Appli
84	6	3.1	127	4	US-09-252-991A-20663	Sequence 20663, A
85	6	3.1	131	3	US-08-772-440-23	Sequence 23, Appli
86	6	3.1	131	3	US-08-772-440-27	Sequence 27, Appli
87	6	3.1	134	3	US-08-772-440-16	Sequence 16, Appli
88	6	3.1	139	3	US-09-422-869-14	Sequence 14, Appli
89	6	3.1	139	3	US-09-543-681A-6177	Sequence 6177, Ap
90	6	3.1	145	3	US-08-772-440-14	Sequence 14, Appli
91	6	3.1	149	4	US-09-489-847-167	Sequence 167, App
92	6	3.1	166	4	US-09-889-914B-8	Sequence 8, Appli
93	6	3.1	167	3	US-08-772-440-21	Sequence 21, Appli
94	6	3.1	168	3	US-08-772-440-17	Sequence 17, Appli
95	6	3.1	168	3	US-09-107-532A-6863	Sequence 6863, Ap
96	6	3.1	170	4	US-09-198-452A-1150	Sequence 1150, Ap
97	6	3.1	171	3	US-09-382-155-23	Sequence 23, Appli
98	6	3.1	171	3	US-09-074-044A-23	Sequence 23, Appli
99	6	3.1	171	4	US-09-205-258-1088	Sequence 1088, Ap
100	6	3.1	175	3	US-08-772-440-15	Sequence 15, Appli

us-10-621-401-145.oligo.rai

Mon May 17 11:51:01 2004

101	6	3.1	180	4	US-08-630-915A-196	Sequence 196, Appl	174
102	6	3.1	180	6	5273901-7	Patent No. 5273901	175
103	6	3.1	180	6	5482709-6	Patent No. 5482709	176
104	6	3.1	182	4	US-09-543-681A-6578	Sequence 6578, Appl	177
105	6	3.1	186	3	US-08-655-359-8	Sequence 8, Appli	178
106	6	3.1	186	4	US-09-258-016-8	Sequence 8, Appli	179
107	6	3.1	186	4	US-09-257-825B-8	Sequence 8, Appli	180
108	6	3.1	187	4	US-09-489-039A-13324	Sequence 13324, A	181
109	6	3.1	187	4	US-09-489-039A-13324	Sequence 107, Appl	182
110	6	3.1	189	4	US-09-328-273-107	Sequence 4645, Ap	183
111	6	3.1	192	4	US-08-772-440-4	Sequence 4, Appli	184
112	6	3.1	209	3	US-09-252-991A-31712	Sequence 31712, A	185
113	6	3.1	210	4	US-09-489-039A-14129	Sequence 14129, A	186
114	6	3.1	212	3	US-08-861-774E-42	Sequence 42, Appl	187
115	6	3.1	214	3	US-09-717-364A-17	Sequence 17, Appl	188
116	6	3.1	218	3	US-09-154-874-2	Sequence 2, Appli	189
117	6	3.1	218	4	US-08-931-668-2	Sequence 2, Appli	190
118	6	3.1	218	4	US-09-543-681A-4533	Sequence 4533, Ap	191
119	6	3.1	218	4	US-09-468-175-2	Sequence 2, Appli	192
120	6	3.1	224	3	US-09-154-874-3	Sequence 3, Appli	193
121	6	3.1	224	3	US-08-931-668-3	Sequence 3, Appli	194
122	6	3.1	224	4	US-09-468-175-3	Sequence 3, Appli	195
123	6	3.1	227	4	US-09-107-532A-6769	Sequence 6769, Ap	196
124	6	3.1	230	2	US-09-702-953B-10	Sequence 10, Appl	197
125	6	3.1	230	2	US-08-537-400-16	Sequence 16, Appl	198
126	6	3.1	230	2	US-08-706-706-18	Sequence 18, Appl	199
127	6	3.1	230	2	US-08-706-706-18	Sequence 18, Appl	200
128	6	3.1	231	4	US-09-238-471-18	Sequence 18, Appl	201
129	6	3.1	231	4	US-09-724-623-116	Sequence 116, Appl	202
130	6	3.1	237	4	US-09-482-273-198	Sequence 198, Appl	203
131	6	3.1	240	2	US-08-114-555A-8	Sequence 6, Appli	204
132	6	3.1	240	2	US-08-114-555A-8	Sequence 12, Appl	205
133	6	3.1	240	3	US-08-559-397A-14	Sequence 14, Appl	206
134	6	3.1	240	3	US-08-559-397A-14	Sequence 14, Appl	207
135	6	3.1	241	3	US-09-961-083-46	Sequence 46, Appl	208
136	6	3.1	241	4	US-09-328-352-6873	Sequence 6873, Ap	209
137	6	3.1	241	4	US-09-536-784-46	Sequence 46, Appl	210
138	6	3.1	241	4	US-08-220-602B-20	Sequence 20, Appl	211
139	6	3.1	257	4	US-09-489-039A-12553	Sequence 12553, A	212
140	6	3.1	260	4	US-09-252-991A-20987	Sequence 20987, A	213
141	6	3.1	267	4	US-09-172-699-18	Sequence 18, Appl	214
142	6	3.1	284	4	US-09-543-681A-6058	Sequence 6058, Ap	215
143	6	3.1	288	4	US-09-252-991A-17252	Sequence 17252, A	216
144	6	3.1	295	4	US-09-252-991A-22439	Sequence 22439, A	217
145	6	3.1	297	1	US-07-866-560-6	Sequence 6, Appli	218
146	6	3.1	297	1	US-08-077-673-6	Sequence 6, Appli	219
147	6	3.1	297	1	US-08-478-992-6	Sequence 6, Appli	220
148	6	3.1	297	3	US-09-105-298-6	Sequence 6, Appli	221
149	6	3.1	297	3	US-08-706-281A-10	Sequence 10, Appl	222
150	6	3.1	297	3	US-09-097-231-10	Sequence 10, Appl	223
151	6	3.1	297	3	US-09-542-122-6	Sequence 6, Appli	224
152	6	3.1	297	4	US-09-303-093-10	Sequence 10, Appl	225
153	6	3.1	298	2	US-09-303-093-3	Sequence 3, Appli	226
154	6	3.1	302	4	US-09-328-352-7673	Sequence 7673, Ap	227
155	6	3.1	303	4	US-09-328-352-7717	Sequence 7717, Ap	228
156	6	3.1	306	4	US-09-674-529B-2	Sequence 2, Appli	229
157	6	3.1	306	4	US-09-489-039A-9175	Sequence 9175, Ap	230
158	6	3.1	315	4	US-09-489-039A-91	Sequence 91, Appl	231
159	6	3.1	315	4	US-09-674-529B-6	Sequence 6, Appli	232
160	6	3.1	315	4	US-09-151-771B-10	Sequence 10, Appl	233
161	6	3.1	317	4	US-09-252-991A-22776	Sequence 22776, A	234
162	6	3.1	321	4	US-09-489-039A-13361	Sequence 13361, A	235
163	6	3.1	324	4	US-09-352-991A-22109	Sequence 22109, A	236
164	6	3.1	325	4	US-09-107-532A-4900	Sequence 4900, Ap	237
165	6	3.1	325	4	US-08-240-049B-13	Sequence 13, Appl	238
166	6	3.1	327	1	US-08-240-049B-14	Sequence 14, Appl	239
167	6	3.1	327	1	US-08-259-148A-15	Sequence 15, Appl	240
168	6	3.1	327	1	US-08-259-148A-16	Sequence 16, Appl	241
169	6	3.1	327	1	US-08-484-054-15	Sequence 15, Appl	242
170	6	3.1	327	1	US-08-484-054-16	Sequence 16, Appl	243
171	6	3.1	327	2	US-07-876-941A-15	Sequence 15, Appl	244
172	6	3.1	327	2	US-07-876-941A-16	Sequence 16, Appl	245
173	6	3.1	327	3	US-08-542-634-17	Sequence 17, Appl	246
174	6	3.1	327	3	US-08-542-634-18	Sequence 18, Appl	247
175	6	3.1	327	3	US-08-477-292-17	Sequence 17, Appl	248
176	6	3.1	327	3	US-08-477-292-18	Sequence 18, Appl	249
177	6	3.1	327	3	US-07-870-985A-15	Sequence 15, Appl	250
178	6	3.1	327	4	US-07-870-985A-16	Sequence 16, Appl	251
179	6	3.1	327	5	PCT-US95-13703-17	Sequence 17, Appl	252
180	6	3.1	327	5	PCT-US95-13703-18	Sequence 18, Appl	253
181	6	3.1	327	5	PCT-US95-13703-18	Sequence 18, Appl	254
182	6	3.1	328	4	US-09-252-991A-31818	Sequence 10, Appl	255
183	6	3.1	329	2	US-08-619-362A-10	Sequence 203, App	256
184	6	3.1	330	3	US-08-851-843A-203	Sequence 322, App	257
185	6	3.1	330	3	US-08-974-549A-322	Sequence 203, App	258
186	6	3.1	330	3	US-08-854-050-203	Sequence 203, App	259
187	6	3.1	330	3	US-09-430-323-203	Sequence 322, App	260
188	6	3.1	330	4	US-09-402-181B-322	Sequence 322, App	261
189	6	3.1	330	4	US-09-721-456-332	Sequence 6, Appli	262
190	6	3.1	334	2	US-08-566-096A-6	Sequence 6, Appli	263
191	6	3.1	334	2	US-08-668-650B-6	Sequence 6, Appli	264
192	6	3.1	334	2	US-08-883-526-4	Sequence 4, Appli	265
193	6	3.1	334	4	US-09-200-673-6	Sequence 6, Appli	266
194	6	3.1	334	4	US-09-194-895-6	Sequence 6, Appli	267
195	6	3.1	334	4	US-09-519-283-4	Sequence 4, Appli	268
196	6	3.1	334	4	US-09-447-907-6	Sequence 6, Appli	269
197	6	3.1	334	5	PCT-US95-15646-6	Sequence 6, Appli	270
198	6	3.1	338	3	US-09-188-930-325	Sequence 325, App	271
199	6	3.1	338	4	US-09-312-283C-325	Sequence 92, Appl	272
200	6	3.1	341	2	US-08-846-762-92	Sequence 33006, A	273
201	6	3.1	347	4	US-09-252-991A-31325	Sequence 31325, A	274
202	6	3.1	352	4	US-09-252-991A-31325	Sequence 2, Appli	275
203	6	3.1	359	2	US-08-713-636-2	Sequence 2, Appli	276
204	6	3.1	360	4	US-09-252-991A-17958	Sequence 17958, A	277
205	6	3.1	361	3	US-09-120-365-75	Sequence 75, Appl	278
206	6	3.1	361	3	US-09-515-039-75	Sequence 75, Appl	279
207	6	3.1	371	3	US-09-252-991A-25766	Sequence 25766, A	280
208	6	3.1	371	3	US-09-252-991A-25766	Sequence 23727, A	281
209	6	3.1	382	4	US-09-252-991A-23727	Sequence 1, Appli	282
210	6	3.1	384	4	US-08-935-887-1	Sequence 36, Appl	283
211	6	3.1	392	1	US-09-464-535-36	Sequence 2, Appli	284
212	6	3.1	394	3	US-08-663-713A-2	Sequence 2, Appli	285
213	6	3.1	394	3	US-09-014-888-2	Sequence 2, Appli	286
214	6	3.1	406	4	US-10-013-846-17	Sequence 17, Appl	287
215	6	3.1	415	2	US-09-247-155-113	Sequence 113, App	288
216	6	3.1	415	2	US-07-667-276A-4	Sequence 7662, Ap	289
217	6	3.1	415	2	US-08-815-718-2	Sequence 4, Appli	290
218	6	3.1	415	4	US-08-854-549A-9	Sequence 9, Appli	291
219	6	3.1	418	4	US-09-328-352-8089	Sequence 8089, Ap	292
220	6	3.1	420	4	US-09-252-991A-25649	Sequence 25649, A	293
221	6	3.1	422	4	US-09-252-991A-19232	Sequence 19232, A	294
222	6	3.1	427	3	US-08-705-771-16	Sequence 16, Appl	295
223	6	3.1	427	3	US-09-417-540-16	Sequence 16, Appl	296
224	6	3.1	428	4	US-09-173-300-36	Sequence 36, Appl	297
225	6	3.1	433	4	US-09-252-991A-23792	Sequence 23792, A	298
226	6	3.1	435	1	US-08-259-148A-18	Sequence 18, Appl	299
227	6	3.1	435	1	US-08-484-054-18	Sequence 18, Appl	300
228	6	3.1	435	2	US-07-876-941A-18	Sequence 18, Appl	301
229	6	3.1	435	2	US-07-876-941A-18	Sequence 18, Appl	302
230	6	3.1	436	1	US-08-259-148A-17	Sequence 17, Appl	303
231	6	3.1	436	1	US-08-484-054-17	Sequence 17, Appl	304
232	6	3.1	436	2	US-07-876-941A-17	Sequence 17, Appl	305
233	6	3.1	436	2	US-07-876-941A-17	Sequence 17, Appl	306
234	6	3.1	437	4	US-09-489-039A-11439	Sequence 11439, A	307
235	6	3.1	438	4	US-09-252-991A-21521	Sequence 21521, A	308
236	6	3.1	439	1	US-08-331-358-10	Sequence 10, Appl	309
237	6	3.1	439	1	US-08-463-694-10	Sequence 10, Appl	310
238	6	3.1	440	2	US-08-694-501-10	Sequence 10, Appl	311
239	6	3.1	440	2	US-08-484-200-4	Sequence 4, Appli	312
240	6	3.1	440	4	US-09-634-238-281	Sequence 281, App	313
241	6	3.1	441	3	US-09-252-991A-22913	Sequence 22913, A	314
242	6	3.1	441	3	US-08-764-870-9	Sequence 9, Appli	315
243	6	3.1	441	3	US-08-980-115-9	Sequence 9, Appli	316
244	6	3.1	441	3	US-09-576-594-1000	Sequence 1000, Ap	317
245	6	3.1	441	4	US-09-173-300-38	Sequence 38, Appl	318
246	6	3.1	445	2	US-08-630-118A-2	Sequence 2, Appli	319
247	6	3.1	445	2	US-08-630-118A-4	Sequence 4, Appli	320

247	6	3.1	445	2	US-08-630-118A-6	Sequence 6, Appli	320	6	3.1	540	4	US-09-854-549A-2	Sequence 2, Appli
248	6	3.1	445	2	US-08-838-399-2	Sequence 2, Appli	321	6	3.1	540	4	US-09-660-107-13	Sequence 13, Appl
249	6	3.1	445	2	US-08-838-399-4	Sequence 4, Appli	322	6	3.1	540	5	PCT-US95-13703-25	Sequence 25, Appl
250	6	3.1	445	2	US-08-838-399-6	Sequence 6, Appli	323	6	3.1	540	5	PCT-US95-13703-26	Sequence 26, Appl
251	6	3.1	445	2	US-09-003-199-2	Sequence 2, Appli	324	6	3.1	548	3	US-08-477-292-16	Sequence 16, Appl
252	6	3.1	445	2	US-09-003-199-21	Sequence 21, Appl	325	6	3.1	549	3	US-08-542-634-15	Sequence 15, Appl
253	6	3.1	445	2	US-09-003-199-23	Sequence 23, Appl	326	6	3.1	549	3	US-08-542-634-16	Sequence 16, Appl
254	6	3.1	445	3	US-09-235-839-2	Sequence 2, Appli	327	6	3.1	549	3	US-08-477-292-15	Sequence 15, Appl
255	6	3.1	445	3	US-09-235-839-4	Sequence 4, Appli	328	6	3.1	549	5	PCT-US95-13703-15	Sequence 15, Appl
256	6	3.1	445	3	US-09-235-839-6	Sequence 6, Appli	329	6	3.1	549	5	PCT-US95-13703-16	Sequence 16, Appl
257	6	3.1	445	3	US-09-040-958-2	Sequence 2, Appli	330	6	3.1	551	2	US-08-700-548-4	Sequence 4, Appli
258	6	3.1	445	3	US-09-040-958-4	Sequence 4, Appli	331	6	3.1	551	2	US-09-172-699-24	Sequence 24, Appl
259	6	3.1	445	4	US-09-327-035-2	Sequence 2, Appli	332	6	3.1	555	4	US-09-134-078-24	Sequence 20, Appl
260	6	3.1	445	4	US-09-327-035-4	Sequence 4, Appli	333	6	3.1	561	4	US-09-172-699-20	Sequence 2, Appli
261	6	3.1	445	4	US-09-065-027-2	Sequence 2, Appli	334	6	3.1	567	4	US-09-957-960-2	Sequence 19751, A
262	6	3.1	445	4	US-09-065-027-4	Sequence 4, Appli	335	6	3.1	568	4	US-09-252-991A-19751	Sequence 26888, A
263	6	3.1	445	4	US-09-065-027-6	Sequence 6, Appli	336	6	3.1	571	3	US-08-484-661A-37	Sequence 37, Appl
264	6	3.1	445	4	US-08-349-025-4	Sequence 4, Appli	337	6	3.1	571	3	US-08-656-664-37	Sequence 37, Appl
265	6	3.1	455	1	US-08-566-096A-4	Sequence 4, Appli	338	6	3.1	571	5	PCT-US96-09641-37	Sequence 4, Appli
266	6	3.1	455	2	US-08-668-650B-4	Sequence 4, Appli	339	6	3.1	574	4	US-09-702-953B-4	Sequence 11, Appl
267	6	3.1	455	2	US-09-200-673-4	Sequence 4, Appli	340	6	3.1	578	3	US-08-484-661A-11	Sequence 11, Appl
268	6	3.1	455	4	US-09-194-895-4	Sequence 4, Appli	341	6	3.1	578	3	US-08-656-664-11	Sequence 11, Appl
269	6	3.1	455	4	US-09-013-846-7	Sequence 4, Appli	342	6	3.1	578	5	PCT-US96-09641-11	Sequence 2, Appli
270	6	3.1	455	4	US-09-447-907-4	Sequence 4, Appli	343	6	3.1	582	4	US-09-428-711A-2	Sequence 2, Appli
271	6	3.1	455	4	US-08-349-025-2	Sequence 2, Appli	344	6	3.1	593	1	US-08-296-362-2	Sequence 8, Appli
272	6	3.1	456	1	US-08-349-025-4	Sequence 4, Appli	345	6	3.1	603	4	US-09-396-149-8	Sequence 32874, A
273	6	3.1	456	2	US-08-566-096A-2	Sequence 2, Appli	346	6	3.1	606	4	US-09-252-991A-32874	Sequence 22263, A
274	6	3.1	456	2	US-08-668-650B-2	Sequence 2, Appli	347	6	3.1	606	4	US-09-252-991A-22263	Sequence 8, Appli
275	6	3.1	456	2	US-08-668-650B-14	Sequence 14, Appl	348	6	3.1	610	3	US-08-484-661A-16	Sequence 16, Appl
276	6	3.1	456	2	US-09-200-673-2	Sequence 2, Appli	349	6	3.1	610	3	US-08-484-661A-19	Sequence 19, Appl
277	6	3.1	456	4	US-03-194-895-2	Sequence 2, Appli	350	6	3.1	610	3	US-08-484-661A-23	Sequence 23, Appl
278	6	3.1	456	4	US-09-194-895-14	Sequence 14, Appl	351	6	3.1	610	3	US-08-484-661A-26	Sequence 26, Appl
279	6	3.1	456	4	US-09-447-907-2	Sequence 2, Appli	352	6	3.1	610	3	US-08-484-661A-29	Sequence 29, Appl
280	6	3.1	456	4	US-09-447-907-14	Sequence 14, Appl	353	6	3.1	610	3	US-08-484-661A-33	Sequence 33, Appl
281	6	3.1	456	5	PCT-US95-15646-2	Sequence 2, Appli	354	6	3.1	610	3	US-08-484-661A-35	Sequence 35, Appl
282	6	3.1	456	5	PCT-US95-15646-4	Sequence 4, Appli	355	6	3.1	610	3	US-08-656-664-8	Sequence 8, Appli
283	6	3.1	462	4	US-09-328-352-4819	Sequence 4819, Ap	356	6	3.1	610	3	US-08-656-664-16	Sequence 16, Appl
284	6	3.1	463	4	US-09-134-000C-4873	Sequence 4873, Ap	357	6	3.1	610	3	US-08-656-664-19	Sequence 19, Appl
285	6	3.1	466	4	US-09-252-991A-27479	Sequence 27479, A	358	6	3.1	610	3	US-08-656-664-23	Sequence 23, Appl
286	6	3.1	468	4	US-09-134-000C-4768	Sequence 4768, Ap	359	6	3.1	610	3	US-08-656-664-26	Sequence 26, Appl
287	6	3.1	470	3	US-08-068-392-2	Sequence 2, Appli	360	6	3.1	610	3	US-08-656-664-29	Sequence 29, Appl
288	6	3.1	470	3	US-08-396-988-2	Sequence 2, Appli	361	6	3.1	610	3	US-08-656-664-33	Sequence 33, Appl
289	6	3.1	470	3	US-09-391-104-26	Sequence 26, Appl	362	6	3.1	610	3	US-08-656-664-35	Sequence 35, Appl
290	6	3.1	476	3	US-09-306-593-9	Sequence 9, Appli	363	6	3.1	610	3	US-08-656-664-35	Sequence 35, Appl
291	6	3.1	477	3	US-09-252-991A-22197	Sequence 22197, A	364	6	3.1	610	3	US-08-656-664-54	Sequence 54, Appl
292	6	3.1	477	4	US-09-446-504-64	Sequence 64, Appl	365	6	3.1	610	3	US-09-019-160-4	Sequence 4, Appli
293	6	3.1	479	3	US-09-712-266-64	Sequence 64, Appl	366	6	3.1	610	4	US-09-019-160-10	Sequence 10, Appl
294	6	3.1	479	3	US-08-484-661A-39	Sequence 39, Appl	367	6	3.1	610	5	PCT-US96-09641-8	Sequence 8, Appli
295	6	3.1	494	3	US-08-656-664-39	Sequence 39, Appl	368	6	3.1	610	5	PCT-US96-09641-16	Sequence 16, Appl
296	6	3.1	494	5	PCT-US96-09641-39	Sequence 13, Appl	369	6	3.1	610	5	PCT-US96-09641-19	Sequence 19, Appl
297	6	3.1	500	4	US-09-265-630-13	Sequence 24948, A	370	6	3.1	610	5	PCT-US96-09641-23	Sequence 23, Appl
298	6	3.1	502	4	US-09-252-991A-24948	Sequence 24948, A	371	6	3.1	610	5	PCT-US96-09641-26	Sequence 26, Appl
299	6	3.1	502	4	US-08-622-191-2	Sequence 2, Appli	372	6	3.1	610	5	PCT-US96-09641-29	Sequence 29, Appl
300	6	3.1	502	4	US-09-323-998B-61	Sequence 61, Appl	373	6	3.1	610	5	PCT-US96-09641-33	Sequence 33, Appl
301	6	3.1	503	4	US-08-857-076-46	Sequence 46, Appl	374	6	3.1	610	5	PCT-US96-09641-35	Sequence 35, Appl
302	6	3.1	503	3	US-08-974-549A-605	Sequence 605, App	375	6	3.1	610	5	PCT-US96-09641-54	Sequence 54, Appl
303	6	3.1	514	3	US-08-912-951-319	Sequence 319, App	376	6	3.1	610	5	US-09-216-393B-81	Sequence 81, Appl
304	6	3.1	514	4	US-09-402-181B-605	Sequence 605, App	377	6	3.1	611	4	US-09-252-991A-19134	Sequence 19134, A
305	6	3.1	514	4	US-09-721-456-605	Sequence 605, App	378	6	3.1	612	4	US-08-295-814B-4	Sequence 4, Appli
306	6	3.1	514	4	US-09-107-532A-6217	Sequence 6217, Ap	379	6	3.1	627	1	US-08-291-299-10	Sequence 10, Appl
307	6	3.1	522	4	US-08-542-634-27	Sequence 27, Appl	380	6	3.1	627	3	US-09-343-361-4	Sequence 4, Appli
308	6	3.1	525	3	US-08-542-634-28	Sequence 28, Appl	381	6	3.1	627	3	US-09-702-953B-3	Sequence 3, Appli
309	6	3.1	525	3	PCT-US95-13703-27	Sequence 27, Appl	382	6	3.1	627	5	PCT-US93-01959-4	Sequence 4, Appli
310	6	3.1	525	3	PCT-US95-13703-28	Sequence 28, Appl	383	6	3.1	627	5	PCT-US93-01959-4	Sequence 10, Appl
311	6	3.1	525	5	US-09-010-147B-20	Sequence 20, Appl	384	6	3.1	627	5	PCT-US93-01959-4	Sequence 10, Appl
312	6	3.1	528	4	US-09-107-532A-6006	Sequence 6006, Ap	385	6	3.1	630	3	US-08-295-814B-10	Sequence 10, Appl
313	6	3.1	533	4	US-09-489-039A-12290	Sequence 12290, A	386	6	3.1	632	3	US-09-343-361-10	Sequence 10, Appl
314	6	3.1	537	4	US-08-884-072-3	Sequence 3, Appli	387	6	3.1	632	5	PCT-US93-01959-10	Sequence 101, App
315	6	3.1	540	2	US-08-542-634-25	Sequence 25, Appl	388	6	3.1	632	3	US-08-857-076-101	Sequence 21770, A
316	6	3.1	540	3	US-08-542-634-26	Sequence 26, Appl	389	6	3.1	635	3	US-09-252-991A-21770	Sequence 95, Appl
317	6	3.1	540	3	US-08-542-634-25	Sequence 25, Appl	390	6	3.1	636	4	US-08-846-762-95	Sequence 2, Appli
318	6	3.1	540	3	US-08-542-634-25	Sequence 25, Appl	391	6	3.1	638	2	US-09-702-953B-2	
319	6	3.1	540	4	US-09-212-168-3	Sequence 3, Appli	392	6	3.1	647	4		

393	6	3.1	659	1	US-08-240-049B-16	Sequence 16, Appl	466	6	3.1	893	4	US-09-019-160-6	Sequence 6, Appli
394	6	3.1	659	1	US-08-259-148A-20	Sequence 20, Appl	467	6	3.1	893	4	US-09-019-160-7	Sequence 7, Appli
395	6	3.1	659	1	US-08-484-054-20	Sequence 20, Appl	468	6	3.1	893	4	US-09-019-160-8	Sequence 8, Appli
396	6	3.1	659	2	US-07-876-941A-20	Sequence 20, Appl	469	6	3.1	893	4	US-09-019-160-9	Sequence 9, Appli
397	6	3.1	659	3	US-08-477-292-14	Sequence 14, Appl	470	6	3.1	893	4	US-09-238-471-3	Sequence 3, Appli
398	6	3.1	659	4	US-07-870-985A-20	Sequence 20, Appl	471	6	3.1	893	5	PCT-US96-08641-2	Sequence 4186, Ap
399	6	3.1	660	1	US-08-240-049B-15	Sequence 15, Appl	472	6	3.1	903	4	US-09-543-881A-4186	Sequence 2, Appli
400	6	3.1	660	1	US-08-259-148A-19	Sequence 19, Appl	473	6	3.1	912	5	PCT-US95-03747-2	Sequence 5208, Ap
401	6	3.1	660	2	US-08-484-054-19	Sequence 19, Appl	474	6	3.1	914	4	US-09-134-001C-5208	Sequence 4, Appli
402	6	3.1	660	1	US-07-876-941A-19	Sequence 19, Appl	475	6	3.1	947	2	US-08-500-857A-4	Sequence 4167, Ap
403	6	3.1	660	3	US-08-840-316-2	Sequence 2, Appli	476	6	3.1	951	4	US-09-328-352-4167	Sequence 27095, A
404	6	3.1	660	3	US-08-478-507-8	Sequence 8, Appli	477	6	3.1	992	4	US-09-252-931A-27095	Sequence 10, Appl
405	6	3.1	660	3	US-08-809-523-2	Sequence 2, Appli	478	6	3.1	1048	4	US-09-171-699-10	Sequence 14, Appl
406	6	3.1	660	3	US-08-542-634-13	Sequence 13, Appl	479	6	3.1	1051	4	US-09-428-711A-14	Sequence 3800, Ap
407	6	3.1	660	3	US-08-542-634-14	Sequence 14, Appl	480	6	3.1	1067	4	US-09-134-001C-3800	Sequence 20, Appl
408	6	3.1	660	3	US-09-128-275A-8	Sequence 8, Appli	481	6	3.1	1102	4	US-09-336-643A-20	Sequence 20, Appl
409	6	3.1	660	3	US-08-471-971-2	Sequence 13, Appl	482	6	3.1	1083	4	US-09-609-776-2	Sequence 2, Appli
410	6	3.1	660	3	US-08-477-292-13	Sequence 8, Appli	483	6	3.1	1083	4	US-09-343-494-1	Sequence 1, Appli
411	6	3.1	660	4	US-09-553-427-8	Sequence 12, Appl	484	6	3.1	1132	3	US-09-358-83C-2	Sequence 3, Appli
412	6	3.1	660	4	US-09-462-606-12	Sequence 12, Appl	485	6	3.1	1132	3	US-08-619-198-3	Sequence 225, App
413	6	3.1	660	4	US-09-462-606-48	Sequence 48, Appl	486	6	3.1	1132	3	US-08-851-843A-225	Sequence 2, Appli
414	6	3.1	660	4	US-09-462-606-49	Sequence 49, Appl	487	6	3.1	1132	3	US-08-974-549A-2	Sequence 344, App
415	6	3.1	660	4	US-09-462-606-50	Sequence 50, Appl	488	6	3.1	1132	3	US-08-974-549A-344	Sequence 225, App
416	6	3.1	660	4	US-09-462-606-52	Sequence 52, Appl	489	6	3.1	1132	3	US-08-854-050-225	Sequence 225, App
417	6	3.1	660	4	US-09-462-606-53	Sequence 53, Appl	490	6	3.1	1132	4	US-09-430-323-225	Sequence 2, Appli
418	6	3.1	660	4	US-09-462-606-54	Sequence 54, Appl	491	6	3.1	1132	4	US-09-128-354-2	Sequence 2, Appli
419	6	3.1	660	4	US-09-462-606-55	Sequence 55, Appl	492	6	3.1	1132	4	US-09-675-321-2	Sequence 2, Appli
420	6	3.1	660	4	US-09-462-606-56	Sequence 56, Appl	493	6	3.1	1132	4	US-09-052-919-2	Sequence 2, Appli
421	6	3.1	660	4	US-09-462-606-57	Sequence 57, Appl	494	6	3.1	1132	4	US-08-912-951-2	Sequence 2, Appli
422	6	3.1	660	4	US-07-870-985A-19	Sequence 19, Appl	495	6	3.1	1132	4	US-09-402-181B-2	Sequence 344, App
423	6	3.1	660	4	US-09-402-776-2	Sequence 2, Appli	496	6	3.1	1132	4	US-09-402-181B-344	Sequence 2, Appli
424	6	3.1	660	5	PCT-US93-08849A-2	Sequence 2, Appli	497	6	3.1	1132	4	US-09-721-456-2	Sequence 344, App
425	6	3.1	660	5	PCT-US93-08849-2	Sequence 2, Appli	498	6	3.1	1132	4	US-09-721-456-344	Sequence 2, Appli
426	6	3.1	660	5	PCT-US95-13703-13	Sequence 13, Appl	499	6	3.1	1132	4	US-09-953-052-2	Sequence 611, App
427	6	3.1	660	5	PCT-US95-13703-14	Sequence 14, Appl	500	6	3.1	1154	3	US-08-974-549A-611	Sequence 323, App
428	6	3.1	672	4	US-09-252-991A-17229	Sequence 17229, A	501	6	3.1	1154	4	US-08-912-951-323	Sequence 611, App
429	6	3.1	677	4	US-09-160-3	Sequence 3, Appli	502	6	3.1	1154	4	US-09-402-181B-611	Sequence 2, Appli
430	6	3.1	680	4	US-09-107-532A-4798	Sequence 4798, Ap	503	6	3.1	1154	4	US-09-721-456-611	Sequence 2, Appli
431	6	3.1	703	4	US-09-252-991A-26000	Sequence 26000, A	504	6	3.1	1158	3	US-09-060-482-2	Sequence 2, Appli
432	6	3.1	708	4	US-09-019-160-5	Sequence 5, Appli	505	6	3.1	1189	3	US-08-974-549A-613	Sequence 613, App
433	6	3.1	713	3	US-09-335-409-11	Sequence 11, Appl	506	6	3.1	1189	4	US-08-912-951-325	Sequence 325, App
434	6	3.1	713	4	US-09-568-102-11	Sequence 11, Appl	507	6	3.1	1189	4	US-09-402-181B-613	Sequence 613, App
435	6	3.1	713	4	US-09-567-969-11	Sequence 11, Appl	508	6	3.1	1200	3	US-09-721-456-613	Sequence 613, App
436	6	3.1	713	4	US-09-568-480-11	Sequence 11, Appl	509	6	3.1	1200	3	US-08-974-549A-612	Sequence 612, App
437	6	3.1	713	4	US-09-568-486-11	Sequence 11, Appl	510	6	3.1	1200	4	US-08-912-951-324	Sequence 612, App
438	6	3.1	713	4	US-09-568-472-11	Sequence 11, Appl	511	6	3.1	1200	4	US-09-402-181B-612	Sequence 612, App
439	6	3.1	713	4	US-09-567-899-11	Sequence 11, Appl	512	6	3.1	1200	4	US-09-721-456-612	Sequence 3, Appli
440	6	3.1	716	4	US-09-616-093-4	Sequence 4, Appli	513	6	3.1	1257	3	US-09-220-641-3	Sequence 600, App
441	6	3.1	735	4	US-09-836-791A-13	Sequence 13, Appl	514	6	3.1	1285	4	US-08-974-549A-600	Sequence 314, App
442	6	3.1	754	4	US-08-941-262-3	Sequence 3, Appli	515	6	3.1	1285	4	US-08-912-951-314	Sequence 600, App
443	6	3.1	754	4	US-08-941-262-3	Sequence 3, Appli	516	6	3.1	1285	4	US-09-402-181B-600	Sequence 600, App
444	6	3.1	755	2	US-09-252-991A-31724	Sequence 31724, A	517	6	3.1	1285	4	US-09-721-456-600	Sequence 5, Appli
445	6	3.1	760	4	US-09-889-914B-2	Sequence 2, Appli	518	6	3.1	1389	2	US-08-619-198-5	Sequence 628, App
446	6	3.1	773	4	US-09-523-849-34	Sequence 34, Appl	519	6	3.1	1407	3	US-08-974-549A-628	Sequence 334, App
447	6	3.1	776	4	US-08-188-228-60	Sequence 60, Appl	520	6	3.1	1407	4	US-08-912-951-334	Sequence 628, App
448	6	3.1	794	1	US-08-332-643-54	Sequence 54, Appl	521	6	3.1	1407	4	US-08-402-181B-628	Sequence 628, App
449	6	3.1	794	1	US-08-332-643-54	Sequence 60, Appl	522	6	3.1	1407	4	US-08-402-181B-628	Sequence 628, App
450	6	3.1	794	1	US-08-332-643-54	Sequence 5, Appli	523	6	3.1	1416	1	US-08-061-465-4	Sequence 4, Appli
451	6	3.1	807	3	US-08-974-549A-5	Sequence 5, Appli	524	6	3.1	1436	2	US-08-652-971-2	Sequence 2, Appli
452	6	3.1	807	4	US-09-402-181B-5	Sequence 5, Appli	525	6	3.1	1436	2	US-08-991-258A-2	Sequence 2, Appli
453	6	3.1	807	4	US-09-402-181B-5	Sequence 5, Appli	526	6	3.1	1436	2	US-08-769-399-2	Sequence 2, Appli
454	6	3.1	807	4	US-09-721-456-5	Sequence 5, Appli	527	6	3.1	1436	2	US-08-991-953A-2	Sequence 2, Appli
455	6	3.1	816	4	US-09-252-991A-28790	Sequence 28790, A	528	6	3.1	1525	3	US-09-191-647-2	Sequence 2, Appli
456	6	3.1	845	4	US-09-641-741-29	Sequence 29, Appl	529	6	3.1	1525	3	US-09-540-245A-2	Sequence 2, Appli
457	6	3.1	851	4	US-09-252-991A-16684	Sequence 16684, A	530	6	3.1	1525	3	US-09-540-153-2	Sequence 2, Appli
458	6	3.1	867	4	US-09-417-485D-2	Sequence 2, Appli	531	6	3.1	1528	1	US-08-463-092B-6	Sequence 6, Appli
459	6	3.1	867	4	US-09-417-485D-4	Sequence 4, Appli	532	6	3.1	1528	2	US-08-462-109A-6	Sequence 6, Appli
460	6	3.1	891	4	US-09-489-039A-11909	Sequence 11909, A	533	6	3.1	1528	2	US-08-460-907B-6	Sequence 6, Appli
461	6	3.1	893	2	US-08-706-702-3	Sequence 3, Appli	534	6	3.1	1528	3	US-08-463-179A-6	Sequence 6, Appli
462	6	3.1	893	3	US-08-484-661A-2	Sequence 2, Appli	535	6	3.1	1529	4	US-08-461-384B-6	Sequence 396, App
463	6	3.1	893	3	US-08-706-706-3	Sequence 3, Appli	536	6	3.1	1529	4	US-09-312-283C-396	Sequence 72, Appl
464	6	3.1	893	3	US-08-656-664-2	Sequence 2, Appli	537	6	3.1	1622	4	US-09-231-899-72	Sequence 8, Appli
465	6	3.1	893	4	US-09-019-160-2	Sequence 2, Appli	538	6	3.1	1786	3	US-08-973-462-8	

539	6	3.1	2125	4	US-09-919-172-29	Sequence 29, Appl	612	5	2.6	19	4	US-09-626-580C-57	Sequence 57, Appl
540	6	3.1	2172	1	US-08-611-107-31	Sequence 31, Appl	613	5	2.6	19	4	US-09-749-959-49	Sequence 49, Appl
541	6	3.1	2257	1	US-08-611-107-10	Sequence 10, Appl	614	5	2.6	20	3	US-09-162-934-13	Sequence 13, Appl
542	6	3.1	2257	3	US-08-422-560A-10	Sequence 10, Appl	615	5	2.6	20	4	US-09-769-180-26	Sequence 26, Appl
543	6	3.1	2257	3	US-08-468-793-10	Sequence 10, Appl	616	5	2.6	21	1	US-08-355-888A-14	Sequence 14, Appl
544	6	3.1	2644	4	US-09-029-047C-2	Sequence 2, Appl	617	5	2.6	21	2	US-08-693-697-14	Sequence 14, Appl
545	5	2.6	5	1	US-07-969-307A-7	Sequence 7, Appl	618	5	2.6	21	3	US-08-693-696-14	Sequence 14, Appl
546	5	2.6	6	1	US-07-969-307A-12	Sequence 12, Appl	619	5	2.6	21	4	US-09-357-914-14	Sequence 14, Appl
547	5	2.6	7	1	US-07-969-307A-16	Sequence 16, Appl	620	5	2.6	21	4	US-09-769-180-23	Sequence 23, Appl
548	5	2.6	7	1	US-07-638-492-14	Sequence 14, Appl	621	5	2.6	21	4	US-09-769-180-24	Sequence 24, Appl
549	5	2.6	7	3	US-09-173-941-34	Sequence 34, Appl	622	5	2.6	21	4	US-09-769-180-25	Sequence 25, Appl
550	5	2.6	7	4	US-09-494-190-34	Sequence 34, Appl	623	5	2.6	21	4	US-09-769-180-27	Sequence 27, Appl
551	5	2.6	8	3	US-08-891-271-3	Sequence 3, Appl	624	5	2.6	22	1	US-08-704-170-30	Sequence 30, Appl
552	5	2.6	8	3	US-08-891-271-9	Sequence 9, Appl	625	5	2.6	22	3	US-08-940-095-31	Sequence 31, Appl
553	5	2.6	8	3	US-08-891-271-12	Sequence 12, Appl	626	5	2.6	22	3	US-08-940-093-31	Sequence 31, Appl
554	5	2.6	8	5	PCT-US95-03236-9	Sequence 9, Appl	627	5	2.6	22	3	US-08-940-096-31	Sequence 31, Appl
555	5	2.6	8	5	US-08-467-083-10	Sequence 10, Appl	628	5	2.6	22	3	US-09-465-719-31	Sequence 31, Appl
556	5	2.6	9	1	US-08-414-417B-10	Sequence 10, Appl	629	5	2.6	22	4	US-09-453-605-31	Sequence 31, Appl
557	5	2.6	9	2	US-08-486-348A-10	Sequence 10, Appl	630	5	2.6	22	4	US-09-453-838-31	Sequence 31, Appl
558	5	2.6	9	2	US-08-468-548B-10	Sequence 10, Appl	631	5	2.6	22	4	US-08-940-136-31	Sequence 31, Appl
559	5	2.6	9	3	US-08-466-680B-10	Sequence 10, Appl	632	5	2.6	22	4	US-09-453-841-31	Sequence 31, Appl
560	5	2.6	9	3	US-09-258-754-335	Sequence 335, App	633	5	2.6	22	4	US-09-453-833-31	Sequence 31, Appl
561	5	2.6	9	3	US-09-042-107-335	Sequence 335, App	634	5	2.6	22	4	US-09-453-826-31	Sequence 31, Appl
562	5	2.6	9	4	US-08-403-459-29	Sequence 29, Appl	635	5	2.6	22	5	PCT-US94-02631-30	Sequence 30, Appl
563	5	2.6	9	4	US-09-722-250D-335	Sequence 335, App	636	5	2.6	23	4	US-09-786-569-18	Sequence 18, Appl
564	5	2.6	9	4	US-09-744-549-31	Sequence 31, Appl	637	5	2.6	24	1	US-08-325-071-30	Sequence 30, Appl
565	5	2.6	9	4	US-09-354-533-10	Sequence 10, Appl	638	5	2.6	24	2	US-08-818-253-32	Sequence 32, Appl
566	5	2.6	10	1	US-08-039-137-27	Sequence 27, Appl	639	5	2.6	24	3	US-08-818-252-32	Sequence 32, Appl
567	5	2.6	10	2	US-08-350-260A-455	Sequence 455, App	640	5	2.6	24	3	US-08-461-004A-30	Sequence 30, Appl
568	5	2.6	10	4	US-09-104-337A-455	Sequence 455, App	641	5	2.6	24	3	US-08-842-322-26	Sequence 26, Appl
569	5	2.6	11	4	US-09-716-129-126	Sequence 126, App	642	5	2.6	24	4	US-09-316-919-48	Sequence 48, Appl
570	5	2.6	12	2	US-08-406-330-50	Sequence 50, Appl	643	5	2.6	25	4	US-09-084-303B-259	Sequence 259, App
571	5	2.6	12	2	US-08-586-597-50	Sequence 50, Appl	644	5	2.6	25	6	5178861-14	Patent No. 5178861
572	5	2.6	12	4	US-08-469-260A-480	Sequence 480, App	645	5	2.6	26	1	US-07-942-245-217	Sequence 217, App
573	5	2.6	12	4	US-08-488-446-480	Sequence 480, App	646	5	2.6	26	1	US-07-942-245-218	Sequence 218, App
574	5	2.6	12	4	US-08-467-344A-480	Sequence 480, App	647	5	2.6	26	1	US-07-942-245-227	Sequence 227, App
575	5	2.6	12	4	US-08-704-170-21	Sequence 21, Appl	648	5	2.6	26	1	US-07-942-245-229	Sequence 229, App
576	5	2.6	13	1	US-08-726-464B-58	Sequence 58, Appl	649	5	2.6	26	2	US-08-690-011A-37	Sequence 37, Appl
577	5	2.6	13	5	PCT-US94-02631-21	Sequence 21, Appl	650	5	2.6	26	2	US-08-690-011A-39	Sequence 39, Appl
578	5	2.6	14	1	US-08-471-780C-46	Sequence 46, Appl	651	5	2.6	26	2	US-08-690-011A-40	Sequence 40, Appl
579	5	2.6	14	1	US-08-467-282B-46	Sequence 46, Appl	652	5	2.6	26	2	US-08-690-011A-41	Sequence 41, Appl
580	5	2.6	14	2	US-08-471-282A-46	Sequence 46, Appl	653	5	2.6	26	2	US-08-690-011A-42	Sequence 42, Appl
581	5	2.6	14	2	US-08-466-710C-46	Sequence 46, Appl	654	5	2.6	26	4	US-09-299-495F-39	Sequence 39, Appl
582	5	2.6	14	3	US-08-468-739C-46	Sequence 46, Appl	655	5	2.6	26	4	US-09-299-495F-37	Sequence 37, Appl
583	5	2.6	14	3	US-09-443-039A-19	Sequence 19, Appl	656	5	2.6	26	4	US-09-299-495F-40	Sequence 40, Appl
584	5	2.6	14	4	US-09-345-624A-11	Sequence 11, Appl	657	5	2.6	26	4	US-09-299-495F-41	Sequence 41, Appl
585	5	2.6	14	4	US-09-331-087D-1	Sequence 1, Appl	658	5	2.6	26	4	US-09-299-495F-42	Sequence 42, Appl
586	5	2.6	14	4	US-09-612-421A-19	Sequence 19, Appl	659	5	2.6	27	1	US-08-124-369-5	Sequence 5, Appl
587	5	2.6	14	6	5445818-6	Patent No. 5445818	660	5	2.6	27	1	US-08-471-780C-31	Sequence 31, Appl
588	5	2.6	15	1	US-07-720-189-5	Sequence 5, Appl	661	5	2.6	27	1	US-08-471-780C-34	Sequence 34, Appl
589	5	2.6	15	1	US-08-467-083-54	Sequence 54, Appl	662	5	2.6	27	1	US-08-467-282B-31	Sequence 31, Appl
590	5	2.6	15	1	US-08-414-417B-54	Sequence 54, Appl	663	5	2.6	27	1	US-08-467-282B-34	Sequence 34, Appl
591	5	2.6	15	2	US-08-486-348A-54	Sequence 54, Appl	664	5	2.6	27	2	US-08-471-282A-31	Sequence 31, Appl
592	5	2.6	15	2	US-08-468-545B-54	Sequence 54, Appl	665	5	2.6	27	2	US-08-471-282A-34	Sequence 34, Appl
593	5	2.6	15	3	US-08-466-680B-54	Sequence 54, Appl	666	5	2.6	27	2	US-08-466-710C-31	Sequence 31, Appl
594	5	2.6	15	3	US-09-205-259-379	Sequence 379, App	667	5	2.6	27	2	US-08-466-710C-34	Sequence 34, Appl
595	5	2.6	15	4	US-09-716-129-127	Sequence 127, App	668	5	2.6	27	2	US-08-620-151-120	Sequence 120, App
596	5	2.6	15	4	US-09-354-533-54	Sequence 54, Appl	669	5	2.6	27	3	US-08-468-739C-31	Sequence 31, Appl
597	5	2.6	17	1	US-08-084-739-8	Sequence 8, Appl	670	5	2.6	27	3	US-08-468-739C-34	Sequence 34, Appl
598	5	2.6	17	1	US-07-638-492-5	Sequence 5, Appl	671	5	2.6	27	3	US-08-818-112-97	Sequence 97, Appl
599	5	2.6	17	1	US-08-146-886-24	Sequence 24, Appl	672	5	2.6	27	4	US-09-056-556-97	Sequence 267, App
600	5	2.6	17	3	US-09-109-613-24	Sequence 24, Appl	673	5	2.6	27	4	US-08-469-260A-267	Sequence 267, App
601	5	2.6	18	1	US-07-690-983D-20	Sequence 20, Appl	674	5	2.6	27	4	US-08-488-446-267	Sequence 267, App
602	5	2.6	18	3	US-08-718-323A-13	Sequence 13, Appl	675	5	2.6	27	4	US-08-467-344A-267	Sequence 267, App
603	5	2.6	18	3	US-08-718-323A-13	Sequence 13, Appl	676	5	2.6	27	4	US-09-072-967-97	Sequence 97, Appl
604	5	2.6	18	3	US-09-077-354B-5	Sequence 5, Appl	677	5	2.6	28	1	US-08-471-780C-39	Sequence 39, Appl
605	5	2.6	18	4	US-09-587-526-11	Sequence 11, Appl	678	5	2.6	28	1	US-08-471-780C-42	Sequence 42, Appl
606	5	2.6	18	4	US-09-587-526-13	Sequence 13, Appl	679	5	2.6	28	1	US-08-467-282B-39	Sequence 39, Appl
607	5	2.6	18	4	US-09-140-749-60	Sequence 60, Appl	680	5	2.6	28	1	US-08-467-282B-42	Sequence 42, Appl
608	5	2.6	18	5	PCT-US93-07653-2	Sequence 2, Appl	681	5	2.6	28	2	US-08-471-282A-39	Sequence 39, Appl
609	5	2.6	19	3	US-09-169-015-52	Sequence 52, Appl	682	5	2.6	28	2	US-08-471-282A-42	Sequence 42, Appl
610	5	2.6	19	4	US-09-626-581D-57	Sequence 57, Appl	683	5	2.6	28	2	US-08-466-710C-39	Sequence 39, Appl
611	5	2.6	19	4	US-09-415-765B-57	Sequence 57, Appl	684	5	2.6	28	2	US-08-466-710C-42	Sequence 42, Appl



us-10-621-401-145.oligo.ra1

Mon May 17 11:51:01 2004

685	5	2.6	28	3	US-08-468-739C-39	Sequence 39, Appl	758	39	4	US-09-834-784-1059	Sequence 1059, Ap
686	5	2.6	28	3	US-08-468-739C-42	Sequence 42, Appl	759	39	4	US-09-515-965A-1059	Sequence 1059, Ap
687	5	2.6	28	3	US-08-941-936-3	Sequence 3, Appl	760	39	4	US-09-350-641C-1059	Sequence 1059, Ap
688	5	2.6	29	2	US-08-470-720-16	Sequence 16, Appl	761	39	5	PCT-US95-1193A-33	Sequence 33, Appl
689	5	2.6	29	2	US-08-867-087B-68	Sequence 68, Appl	762	40	3	US-09-082-279B-969	Sequence 969, App
690	5	2.6	29	2	US-08-469-260A-254	Sequence 254, App	763	40	3	US-09-315-304B-969	Sequence 969, App
691	5	2.6	29	4	US-08-468-446-254	Sequence 254, App	764	40	4	US-09-834-784-969	Sequence 969, App
692	5	2.6	29	4	US-08-467-344A-254	Sequence 254, App	765	40	4	US-09-515-965A-969	Sequence 969, App
693	5	2.6	29	4	US-08-121-054C-19	Sequence 19, Appl	766	40	4	US-09-350-641C-969	Sequence 969, App
694	5	2.6	30	1	US-08-121-054C-20	Sequence 20, Appl	767	41	1	US-08-111-939-27	Sequence 27, Appl
695	5	2.6	30	1	US-08-121-054C-21	Sequence 21, Appl	768	41	1	US-08-475-989-44	Sequence 44, Appl
696	5	2.6	30	1	US-08-121-054C-22	Sequence 22, Appl	769	42	2	US-08-475-985-44	Sequence 44, Appl
697	5	2.6	30	1	US-08-121-054C-26	Sequence 26, Appl	770	42	2	US-08-256-839-44	Sequence 44, Appl
698	5	2.6	30	1	US-08-121-054C-27	Sequence 27, Appl	771	42	3	US-03-167-681-33	Sequence 33, Appl
699	5	2.6	30	2	US-08-598-873-46	Sequence 46, Appl	772	42	3	US-09-167-681-49	Sequence 49, Appl
700	5	2.6	30	3	US-09-141-047-11	Sequence 11, Appl	773	43	1	US-07-998-003A-93	Sequence 93, Appl
701	5	2.6	30	3	US-08-539-436-19	Sequence 19, Appl	774	43	1	US-08-453-274B-93	Sequence 93, Appl
702	5	2.6	30	3	US-08-539-436-20	Sequence 20, Appl	775	43	1	US-08-453-695A-93	Sequence 93, Appl
703	5	2.6	30	3	US-08-539-436-21	Sequence 21, Appl	776	43	1	US-08-268-161A-93	Sequence 93, Appl
704	5	2.6	30	3	US-08-539-436-24	Sequence 24, Appl	777	43	2	US-08-453-702A-93	Sequence 93, Appl
705	5	2.6	30	3	US-08-539-436-26	Sequence 26, Appl	778	43	2	US-09-099-659-93	Sequence 93, Appl
706	5	2.6	30	3	US-08-539-436-27	Sequence 27, Appl	779	43	3	PCT-US93-12588-93	Sequence 93, Appl
707	5	2.6	30	3	US-08-605-430-46	Sequence 46, Appl	780	43	5	PCT-US95-08071-93	Sequence 33, Appl
708	5	2.6	30	4	US-09-813-659-19	Sequence 19, Appl	781	44	3	US-08-888-429A-33	Sequence 33, Appl
709	5	2.6	30	4	US-09-813-659-21	Sequence 21, Appl	782	44	4	US-08-918-148-56	Sequence 56, Appl
710	5	2.6	30	4	US-09-813-659-24	Sequence 24, Appl	783	44	4	US-09-593-653-33	Sequence 33, Appl
711	5	2.6	30	4	US-09-813-659-26	Sequence 26, Appl	784	45	1	US-08-422-101-22	Sequence 22, Appl
712	5	2.6	30	4	US-09-813-659-27	Sequence 27, Appl	785	45	1	US-08-422-091-22	Sequence 22, Appl
713	5	2.6	30	4	US-09-813-659-27	Sequence 27, Appl	786	45	2	US-09-027-449-57	Sequence 57, Appl
714	5	2.6	30	4	US-09-549-067A-19	Sequence 19, Appl	787	45	3	US-08-422-093-22	Sequence 22, Appl
715	5	2.6	30	4	US-09-549-067A-21	Sequence 21, Appl	788	45	3	US-08-804-44A-57	Sequence 57, Appl
716	5	2.6	30	4	US-09-549-067A-24	Sequence 24, Appl	789	45	3	US-08-422-112-22	Sequence 22, Appl
717	5	2.6	30	4	US-09-549-067A-26	Sequence 26, Appl	790	45	3	US-08-422-112-22	Sequence 22, Appl
718	5	2.6	30	4	US-09-549-067A-27	Sequence 27, Appl	791	45	3	US-09-121-952A-57	Sequence 57, Appl
719	5	2.6	30	5	PCT-US92-01196-9	Sequence 9, Appl	792	45	4	US-09-234-340A-57	Sequence 8, Appl
720	5	2.6	32	5	US-09-082-279B-989	Sequence 989, App	793	46	1	US-08-466-127-8	Sequence 8, Appl
721	5	2.6	34	4	US-09-315-304B-989	Sequence 989, App	794	46	4	US-08-936-165A-483	Sequence 483, App
722	5	2.6	34	4	US-09-315-304B-989	Sequence 989, App	795	46	4	US-09-369-247-126	Sequence 126, App
723	5	2.6	34	4	US-09-515-965A-989	Sequence 989, App	796	46	4	US-08-282-197C-44	Sequence 44, Appl
724	5	2.6	34	4	US-09-515-965A-989	Sequence 989, App	797	46	4	US-08-062-472B-46	Sequence 46, Appl
725	5	2.6	34	4	US-09-350-641C-989	Sequence 989, App	798	48	1	US-09-082-279B-970	Sequence 970, App
726	5	2.6	35	1	US-08-471-780C-127	Sequence 127, App	799	48	3	US-09-082-279B-1060	Sequence 1060, Ap
727	5	2.6	35	1	US-08-467-282B-127	Sequence 127, App	800	48	3	US-09-315-304B-970	Sequence 970, App
728	5	2.6	35	2	US-08-471-780C-127	Sequence 127, App	801	48	4	US-09-315-304B-1060	Sequence 1060, Ap
729	5	2.6	35	2	US-08-466-710C-127	Sequence 127, App	802	48	4	US-09-315-304B-1060	Sequence 22, Appl
730	5	2.6	35	2	US-08-468-739C-127	Sequence 127, App	803	48	4	US-09-384-302A-22	Sequence 22, Appl
731	5	2.6	35	3	US-09-183-706-39	Sequence 39, Appl	804	48	4	US-09-834-784-970	Sequence 970, App
732	5	2.6	35	3	US-09-567-995-39	Sequence 39, Appl	805	48	4	US-09-834-784-1060	Sequence 1060, Ap
733	5	2.6	35	4	US-09-205-258-900	Sequence 900, App	806	48	4	US-09-515-965A-970	Sequence 970, App
734	5	2.6	36	1	US-08-487-890A-66	Sequence 66, Appl	807	48	4	PCT-US93-05640-38	Sequence 38, Appl
735	5	2.6	36	1	US-08-039-137-42	Sequence 42, Appl	808	48	4	US-09-515-965A-1060	Sequence 1060, Ap
736	5	2.6	36	2	US-08-478-435-66	Sequence 66, Appl	809	48	4	US-09-350-641C-970	Sequence 970, App
737	5	2.6	36	2	US-08-337-483-66	Sequence 66, Appl	810	48	4	US-09-350-641C-1060	Sequence 1060, Ap
738	5	2.6	36	2	US-08-478-373-66	Sequence 66, Appl	811	49	4	US-09-377-466B-27	Sequence 27, Appl
739	5	2.6	36	3	US-08-478-671-66	Sequence 66, Appl	812	50	2	US-08-799-173A-14	Sequence 14, Appl
740	5	2.6	36	3	US-08-483-577A-66	Sequence 66, Appl	813	50	2	US-08-471-780C-44	Sequence 44, Appl
741	5	2.6	36	3	US-08-897-438-66	Sequence 66, Appl	814	51	4	US-08-471-282A-44	Sequence 44, Appl
742	5	2.6	36	4	US-08-637-654-66	Sequence 66, Appl	815	51	4	US-08-466-710C-44	Sequence 44, Appl
743	5	2.6	36	4	US-08-649-518-66	Sequence 66, Appl	816	51	4	US-08-468-739C-44	Sequence 44, Appl
744	5	2.6	37	2	US-08-807-332B-13	Sequence 13, Appl	817	51	4	US-09-621-976-6682	Sequence 7469, Ap
745	5	2.6	37	3	US-09-338-876-13	Sequence 13, Appl	818	51	4	US-09-621-976-6682	Sequence 7469, Ap
746	5	2.6	38	3	US-09-082-279B-988	Sequence 988, App	819	54	1	US-08-471-780C-44	Sequence 44, Appl
747	5	2.6	38	4	US-09-315-304B-988	Sequence 988, App	820	54	2	US-08-471-282A-44	Sequence 44, Appl
748	5	2.6	38	4	US-09-205-258-435	Sequence 435, App	821	54	2	US-08-466-710C-44	Sequence 44, Appl
749	5	2.6	38	4	US-09-515-965A-988	Sequence 988, App	822	54	3	US-08-468-739C-44	Sequence 44, Appl
750	5	2.6	38	4	US-09-350-641C-988	Sequence 988, App	823	54	4	US-09-621-976-6682	Sequence 7469, Ap
751	5	2.6	38	4	US-09-010-317-37	Sequence 37, Appl	824	55	4	US-09-621-976-6682	Sequence 7469, Ap
752	5	2.6	38	4	US-09-010-317-37	Sequence 37, Appl	825	56	4	US-09-621-976-6682	Sequence 7469, Ap
753	5	2.6	38	4	US-08-488-161-33	Sequence 33, Appl	826	57	4	US-09-621-976-6682	Sequence 7469, Ap
754	5	2.6	39	2	US-09-273-685-33	Sequence 33, Appl	827	58	3	US-08-293-728-4	Sequence 4, Appl
755	5	2.6	39	3	US-09-082-279B-1059	Sequence 1059, Ap	828	58	3	US-09-800-729-168	Sequence 168, App
756	5	2.6	39	3	US-09-082-279B-1059	Sequence 1059, Ap	829	58	4	US-09-621-976-6682	Sequence 6020, Ap
757	5	2.6	39	4	US-09-315-304B-1059	Sequence 1059, Ap	830	59	3	US-08-651-136C-38	Sequence 38, Appl

831 5 2.6 4 US-09-229-911A-38 Sequence 38, Appl 904  
832 5 2.6 4 US-09-621-976-7401 Sequence 7401, Ap 905  
833 5 2.6 1 US-08-471-780C-87 Sequence 87, Appl 906  
834 5 2.6 1 US-08-467-282B-87 Sequence 87, Appl 907  
835 5 2.6 1 US-08-471-282A-87 Sequence 87, Appl 908  
836 5 2.6 2 US-08-466-710C-87 Sequence 87, Appl 909  
837 5 2.6 3 US-08-468-739C-87 Sequence 87, Appl 910  
838 5 2.6 60 US-09-621-976-5555 Sequence 5555, Ap 911  
839 5 2.6 60 US-09-621-976-6003 Sequence 6003, Ap 912  
840 5 2.6 61 US-09-328-352-7170 Sequence 7170, Ap 913  
841 5 2.6 61 US-09-621-976-4504 Sequence 4504, Ap 914  
842 5 2.6 61 5164304-13 Patent No. 5164304 915  
843 5 2.6 63 US-09-621-976-5530 Sequence 5530, Ap 916  
844 5 2.6 63 5182210-14 Patent No. 5182210 917  
845 5 2.6 63 5198542-11 Patent No. 5198542 918  
846 5 2.6 64 US-08-894-626-3 Sequence 3, Appl 919  
847 5 2.6 64 US-09-489-039A-10494 Sequence 10494, A 920  
848 5 2.6 64 US-09-621-976-6883 Sequence 6883, Ap 921  
849 5 2.6 65 US-08-435-040-2 Sequence 2, Appl 922  
850 5 2.6 65 3 US-09-020-216-2 Sequence 2, Appl 923  
851 5 2.6 65 4 US-08-569-147-85 Sequence 85, Appl 924  
852 5 2.6 65 4 US-09-257-179-113 Sequence 113, Ap 925  
853 5 2.6 66 4 US-09-107-532A-6100 Sequence 6100, Ap 926  
854 5 2.6 66 4 US-08-471-780C-126 Sequence 126, Ap 927  
855 5 2.6 67 1 US-08-471-780C-126 Sequence 126, Ap 928  
856 5 2.6 67 1 US-08-467-282B-126 Sequence 126, Ap 929  
857 5 2.6 67 2 US-08-466-710C-126 Sequence 126, Ap 930  
858 5 2.6 67 2 US-08-468-739C-126 Sequence 126, Ap 931  
859 5 2.6 67 3 US-09-252-991A-22054 Sequence 22054, A 932  
860 5 2.6 67 4 US-09-543-681A-7835 Sequence 7835, Ap 933  
861 5 2.6 67 4 US-09-134-000C-6554 Sequence 6554, Ap 934  
862 5 2.6 67 4 US-09-134-000C-6707 Sequence 6707, Ap 935  
863 5 2.6 68 4 US-09-527-236A-23 Sequence 23, Appl 936  
864 5 2.6 68 4 US-09-328-352-7550 Sequence 7550, Ap 937  
865 5 2.6 68 4 US-09-621-976-5340 Sequence 5340, Ap 938  
866 5 2.6 68 4 US-09-756-854-23 Sequence 23, Appl 939  
867 5 2.6 70 3 US-08-911-321-7 Sequence 7, Appl 940  
868 5 2.6 70 4 US-09-123-144-15 Sequence 15, Appl 941  
869 5 2.6 70 4 US-09-205-258-1160 Sequence 1160, Ap 942  
870 5 2.6 70 4 US-09-159-277A-6 Sequence 6, Appl 943  
871 5 2.6 70 4 US-09-732-210-1105 Sequence 1105, Ap 944  
872 5 2.6 70 4 US-09-489-039A-14233 Sequence 14233, A 945  
873 5 2.6 70 4 US-09-621-976-5534 Sequence 5534, Ap 946  
874 5 2.6 71 3 US-09-621-976-5534 Sequence 23, Appl 947  
875 5 2.6 71 4 US-09-621-976-5534 Sequence 24, Appl 948  
876 5 2.6 71 4 US-09-230-041-25 Sequence 25, Appl 949  
877 5 2.6 71 4 US-09-230-041-25 Sequence 23, Appl 950  
878 5 2.6 71 4 US-09-637-240-23 Sequence 67, Appl 951  
879 5 2.6 71 4 US-09-637-240-23 Sequence 5381, Ap 952  
880 5 2.6 71 4 US-09-621-976-7737 Sequence 7737, Ap 953  
881 5 2.6 72 4 US-09-621-976-7737 Sequence 7737, Ap 954  
882 5 2.6 72 4 US-09-621-976-7737 Sequence 7585, Ap 955  
883 5 2.6 72 4 US-09-621-976-7737 Sequence 213, Ap 956  
884 5 2.6 74 4 US-08-894-139-5 Sequence 5, Appl 957  
885 5 2.6 74 1 US-08-428-415-18 Sequence 18, Appl 958  
886 5 2.6 75 1 US-08-379-685-18 Sequence 18, Appl 959  
887 5 2.6 75 2 US-08-854-029-18 Sequence 18, Appl 960  
888 5 2.6 75 3 US-08-428-762-18 Sequence 18, Appl 961  
889 5 2.6 75 4 US-09-227-357-299 Sequence 299, Ap 962  
890 5 2.6 76 4 US-09-198-452A-1261 Sequence 1261, A 963  
891 5 2.6 76 4 US-09-543-681A-6797 Sequence 6797, Ap 964  
892 5 2.6 76 4 US-09-621-976-6694 Sequence 6694, Ap 965  
893 5 2.6 76 4 US-09-621-976-6797 Sequence 6797, Ap 966  
894 5 2.6 76 4 US-09-621-976-7706 Sequence 7706, Ap 967  
895 5 2.6 77 4 US-08-924-629C-27 Sequence 27, Appl 968  
896 5 2.6 77 4 US-08-924-629C-28 Sequence 28, Appl 969  
897 5 2.6 77 4 US-09-255-518C-15 Sequence 15, Appl 970  
898 5 2.6 77 4 US-09-255-518C-38 Sequence 38, Appl 971  
899 5 2.6 77 4 US-09-255-518C-40 Sequence 40, Appl 972  
900 5 2.6 77 4 US-09-393-634-11 Sequence 11, Appl 973  
901 5 2.6 77 4 US-09-621-976-4259 Sequence 4259, Ap 974  
902 5 2.6 77 4 US-09-540-236-3650 Sequence 3650, Ap 975  
903 5 2.6 78 2 US-07-885-089B-30 Sequence 30, Appl 976

78 2 US-07-885-089B-32 Sequence 32, Appl 32  
78 4 US-09-149-476-356 Sequence 356, Ap 36  
78 4 US-08-828-683A-23 Sequence 23, Appl 33  
79 2 US-07-885-089B-33 Sequence 33, Appl 34  
79 4 US-09-134-001C-3727 Sequence 3727, Ap 35  
79 4 US-09-186-002-4 Sequence 4, Appl 36  
79 4 US-09-377-468B-26 Sequence 26, Appl 37  
79 4 US-09-252-991A-31631 Sequence 31631, A 38  
79 4 US-09-247-155-93 Sequence 93, Appl 39  
80 4 US-09-252-991A-26748 Sequence 26748, A 40  
80 4 US-09-107-532A-5588 Sequence 5588, Ap 41  
80 4 US-09-489-039A-13031 Sequence 13031, A 42  
80 4 US-09-564-805-211 Sequence 211, Ap 43  
81 4 US-09-107-532A-4732 Sequence 4732, Ap 44  
81 4 US-09-543-681A-5027 Sequence 5027, Ap 45  
81 4 US-09-084-303B-159 Sequence 159, Ap 46  
81 4 US-08-483-577A-160 Sequence 160, Ap 47  
82 3 US-08-897-438-160 Sequence 160, Ap 48  
82 4 US-08-649-518-160 Sequence 160, Ap 49  
82 4 US-09-134-000C-3837 Sequence 3837, Ap 50  
82 4 US-08-370-225-23 Sequence 23, Appl 51  
83 1 US-07-885-089B-16 Sequence 16, Appl 52  
83 1 US-07-885-089B-18 Sequence 18, Appl 53  
83 2 US-07-791-931-3 Sequence 3, Appl 54  
83 3 US-08-305-223-458 Sequence 458, Ap 55  
83 3 US-09-222-575-62 Sequence 62, Appl 56  
83 4 US-09-389-681-62 Sequence 62, Appl 57  
83 4 US-09-620-405B-62 Sequence 229, Ap 58  
83 4 US-09-732-210-229 Sequence 62, Appl 59  
83 4 US-09-339-338-62 Sequence 62, Appl 60  
83 4 US-09-433-826B-62 Sequence 62, Appl 61  
83 4 US-09-604-287A-62 Sequence 62, Appl 62  
83 4 US-09-285-480-62 Sequence 62, Appl 63  
83 4 US-09-834-759-62 Sequence 23, Appl 64  
84 5 PCT-US93-10069-23 Sequence 23, Appl 65  
84 5 US-09-328-352-6298 Sequence 6298, Ap 66  
84 5 US-09-069-827A-120 Sequence 120, Ap 67  
84 6 5202428-10 Patent No. 5202428 68  
85 4 US-09-247-155-123 Sequence 123, Ap 69  
85 4 US-09-732-210-1104 Sequence 1104, Ap 70  
85 4 US-09-079-030-36 Sequence 36, Appl 71  
85 4 US-09-621-976-5559 Sequence 5559, Ap 72  
85 4 US-09-621-976-5559 Sequence 6444, Ap 73  
85 4 US-09-621-976-5559 Sequence 5, Appl 74  
86 3 US-09-042-785A-25 Sequence 25, Appl 75  
86 4 US-09-107-532A-5983 Sequence 5983, Ap 76  
86 4 US-09-540-236-3805 Sequence 3805, Ap 77  
86 4 US-08-308-086-11 Sequence 11, Appl 78  
86 4 US-09-328-352-6117 Sequence 6117, Ap 79  
86 4 US-09-543-681A-6772 Sequence 6772, Ap 80  
88 4 US-09-621-976-3949 Sequence 3949, Ap 81  
88 4 US-09-621-976-5007 Sequence 5007, Ap 82  
88 4 US-09-621-976-7479 Sequence 7479, Ap 83  
88 4 US-09-621-976-7479 Sequence 22, Appl 84  
89 1 US-08-167-035-22 Sequence 22, Appl 85  
89 1 US-08-208-887A-22 Sequence 16, Appl 86  
89 2 US-08-479-078-16 Sequence 22, Appl 87  
89 2 US-08-539-005-22 Sequence 22, Appl 88  
89 4 US-09-280-598-24 Sequence 24, Appl 89  
89 4 US-09-621-976-5346 Sequence 5346, Ap 90  
89 4 US-09-333-803-100 Sequence 100, Ap 91  
89 4 US-09-540-236-3747 Sequence 3747, Ap 92  
89 4 US-09-205-258-357 Sequence 357, Ap 93  
90 4 US-09-393-634-76 Sequence 76, Appl 94  
90 4 US-09-732-210-1178 Sequence 1178, Ap 95  
90 4 US-09-732-210-1180 Sequence 1180, Ap 96  
90 4 US-09-732-210-1182 Sequence 1182, Ap 97  
90 4 US-09-621-976-4252 Sequence 4252, Ap 98  
91 3 US-09-077-977A-1 Sequence 1, Appl 99  
91 3 US-09-252-991A-26453 Sequence 26453, A 100  
91 4 US-09-107-532A-6647 Sequence 6647, Ap 101  
91 4 US-09-621-976-7015 Sequence 7015, Ap 102  
92 4 US-09-205-258-890 Sequence 890, Ap 103



us-10-621-401-145.oligo.ra1

Mon May 17 11:51:01 2004

Sequence 11, Appl  
Sequence 7121, Ap  
Sequence 31, Appl  
Sequence 25156, A  
Sequence 12, Appl  
Sequence 106, Appl  
Sequence 11, Appl  
Sequence 381, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 381, Appl  
Sequence 40, Appl  
Sequence 1175, Ap  
Sequence 3, Appl  
Sequence 9, Appl  
Sequence 15, Appl  
Sequence 2, Appl  
Sequence 23, Appl  
Sequence 2, Appl  
Sequence 13, Appl  
Sequence 18, Appl  
Sequence 4212, Ap  
Sequence 4, Appl  
Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-155-171B-16  
; Sequence 16, Application US/08155171B  
; Patent No. 5543264  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Carl W.  
; APPLICANT: Mangel, Walter F.  
; TITLE OF INVENTION: Co-Factor Activated Recombinant  
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/155,171B  
FILING DATE: 19-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/851,217  
FILING DATE: 13-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/545,585  
FILING DATE: 29-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: linear  
US-08-155-171B-16

Query Match 4.1%; Score 8; DB 1; Length 214;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GCGSYFLG 94  
|||  
Db 16 GCGSYFLG 23

RESULT 2  
US-08-435-998-16  
; Sequence 16, Application US/08435998  
; Patent No. 5935840  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Carl W.  
; APPLICANT: Mangel, Walter F.  
; TITLE OF INVENTION: Co-Factor Activated Recombinant  
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,998  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,171  
FILING DATE: 19-NOV-1993  
APPLICATION NUMBER: US 07/851,217  
FILING DATE: 13-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/545,585  
FILING DATE: 29-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-435-998-16

Query Match 4.1%; Score 8; DB 2; Length 214;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GCGSYFLG 94  
|||  
Db 16 GCGSYFLG 23

RESULT 3  
US-08-038-343A-5  
; Sequence 5, Application US/08038343A

Patent No. 5427928  
GENERAL INFORMATION:  
APPLICANT: Slesarev, Alexei I  
TITLE OF INVENTION: Thermostable Prokaryotic DNA  
TITLE OF INVENTION: Topoisomerase V  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 11150 Santa Monica Boulevard, Suite 400  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/038,343A  
FILING DATE: 24-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9727  
TELEPHONE: (310) 445-1140  
TELEFAX: (310) 445-9031  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Methanopyrus kandleri  
US-08-038-343A-5

Query Match 3.6%; Score 7; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194  
Db 10 EEEKEEL 16

RESULT 4  
US-08-185-414E-4  
Sequence 4, Application US/08185414E  
Patent No. 5556953  
GENERAL INFORMATION:  
APPLICANT: Zhang, Lei  
APPLICANT: Vijay, Hari M.  
TITLE OF INVENTION: ALLERGEN OF CLADOSPORIUM HERBARUM  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: George A. Seaby  
ADDRESSEE: Seaby and Maclean  
STREET: 880 Wellington Street, Suite 708  
CITY: Ottawa  
COUNTRY: Canada  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/185,414E

FILING DATE: January 24, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George A. Seaby  
REGISTRATION NUMBER: 24,034  
REFERENCE/DOCKET NUMBER: 1747  
TELEPHONE: (613) 232-5815  
TELEFAX: (613) 232-5831  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: yeast ribosomal P2 protein  
LOCATION: 1...106  
US-08-185-414E-4

Query Match 3.6%; Score 7; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 AEEKEE 193  
Db 84 AEEKEE 90

RESULT 5  
US-09-250-609-2  
Sequence 2, Application US/09250609A  
Patent No. 6458943  
GENERAL INFORMATION:  
APPLICANT: Byrnie, Jennifer A.  
TITLE OF INVENTION: Members of the D52 Gene Family  
FILE REFERENCE: 1383.0210002  
CURRENT APPLICATION NUMBER: US/09/250,609A  
CURRENT FILING DATE: 1999-02-17  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-250-609-2

Query Match 3.6%; Score 7; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194  
Db 46 EEEKEEL 52

RESULT 6  
US-09-250-611-2  
Sequence 2, Application US/09250611  
Patent No. 6528283  
GENERAL INFORMATION:  
APPLICANT: Byrnie, Jennifer A.  
APPLICANT: Basset, Paul  
TITLE OF INVENTION: Members of the D52 Gene Family  
FILE REFERENCE: 1383.0210001  
CURRENT APPLICATION NUMBER: US/09/250,611  
CURRENT FILING DATE: 1999-02-17  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 144  
TYPE: PRT

us-10-621-401-145.oligo.ra1

Mon May 17 11:51:01 2004

```

; ORGANISM: Homo sapiens
US-09-250-611-2
Query Match 3.6%; Score 7; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194
Db 46 EEEKEEL 52

RESULT 7
US-09-216-393B-73
; Sequence 73, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 73
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-73

Query Match 3.6%; Score 7; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 RSLGFVS 152
Db 62 RSLGFVS 68

RESULT 8
US-09-134-000C-3705
; Sequence 3705, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3705
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3705

Query Match 3.6%; Score 7; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 ESMDLGI 105
Db 72 ESMDLGI 78

RESULT 9
US-08-715-204-1
; Sequence 1, Application US/08715204
; Patent No. 5874286
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer.
; APPLICANT: Zweiger, Gary B.
; TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,204
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0126 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-715-204-1

Query Match 3.6%; Score 7; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194
Db 33 EEEKEEL 39

RESULT 10
US-08-691-814B-10
; Sequence 10, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Bassett, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC

```

us-10-621-401-145.oligo.ra1

Mon May 17 11:51:01 2004

COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/691,814B  
 FILING DATE: 31-JUL-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/002,183  
 FILING DATE: 09-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Steffe, Eric K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1383.0090001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2543  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 204 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-691-814B-10

Query Match 3.6%; Score 7; DB 2; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194  
 Db 33 EEEKEEL 39  
 |||||

RESULT 11  
 US-09-162-597-1  
 ; Sequence 1, Application US/09162597  
 ; Patent No. 6043343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Goli, Surya K.  
 ; APPLICANT: Hillman, Jennifer.  
 ; APPLICANT: Zweiger, Gary B.  
 ; TITLE OF INVENTION: A NOVEL TUMOR PROTEIN  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/162,597  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/715,204  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0126 US  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 204 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: Consensus  
 CLONE: Consensus  
 US-09-162-597-1

Query Match 3.6%; Score 7; DB 3; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194  
 Db 33 EEEKEEL 39  
 |||||

RESULT 12  
 US-09-250-609-4  
 ; Sequence 4, Application US/09250609A  
 ; Patent No. 6458943  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Byrne, Jennifer A.  
 ; TITLE OF INVENTION: Members of the D52 Gene Family  
 ; FILE REFERENCE: 1383.0210002  
 ; CURRENT APPLICATION NUMBER: US/09/250,609A  
 ; CURRENT FILING DATE: 1999-02-17  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 204  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-250-609-4

Query Match 3.6%; Score 7; DB 4; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194  
 Db 33 EEEKEEL 39  
 |||||

RESULT 13  
 US-09-250-609-9  
 ; Sequence 9, Application US/09250609A  
 ; Patent No. 6458943  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Byrne, Jennifer A.  
 ; TITLE OF INVENTION: Members of the D52 Gene Family  
 ; FILE REFERENCE: 1383.0210002  
 ; CURRENT APPLICATION NUMBER: US/09/250,609A  
 ; CURRENT FILING DATE: 1999-02-17  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 204  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-250-609-9

Query Match 3.6%; Score 7; DB 4; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194

Db 33 EEEKEEL 39

RESULT 14  
US-09-250-611-4  
; Sequence 4, Application US/09250611  
; Patent No. 6528283  
; GENERAL INFORMATION:  
; APPLICANT: Byrnie, Jennifer A.  
; APPLICANT: Bassett, Paul  
; TITLE OF INVENTION: Members of the D52 Gene Family  
; FILE REFERENCE: 1383.0210001  
; CURRENT APPLICATION NUMBER: US/09/250,611  
; CURRENT FILING DATE: 1999-02-17  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-250-611-4

Query Match 3.6%; Score 7; DB 4; Length 204;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194  
Db 33 EEEKEEL 39

RESULT 15  
US-09-250-611-9  
; Sequence 9, Application US/09250611  
; Patent No. 6528283  
; GENERAL INFORMATION:  
; APPLICANT: Byrnie, Jennifer A.  
; APPLICANT: Bassett, Paul  
; TITLE OF INVENTION: Members of the D52 Gene Family  
; FILE REFERENCE: 1383.0210001  
; CURRENT APPLICATION NUMBER: US/09/250,611  
; CURRENT FILING DATE: 1999-02-17  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-250-611-9

Query Match 3.6%; Score 7; DB 4; Length 204;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194  
Db 33 EEEKEEL 39

Search completed: May 17, 2004, 10:53:37  
Job time : 32 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:53:06 ; Search time 45 Seconds  
(without alignments)  
1199.616 Million cell updates/sec

US-10-621-401-145

Perfect score: 194

Sequence: 1 MKLASGFLVLSLGGGLAQ.....PFMSQRAACIABEKEKEL 194

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1145568 seqs, 278261457 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.5	194	10	US-09-974-879-145
2	193	99.5	194	12	US-10-621-401-145
3	193	99.5	195	10	US-09-305-736-144
4	193	99.5	195	11	US-09-818-683-144
5	137	70.6	194	12	US-10-363-616-357
6	8	4.1	194	9	US-09-975-374A-13
7	8	4.1	306	12	US-10-425-114-45178
8	8	4.1	484	14	US-10-156-761-13394
9	8	4.1	679	12	US-10-425-114-51651
10	8	4.1	780	12	US-10-425-114-56183
11	7	3.6	34	10	US-09-774-639-334
12	7	3.6	34	10	US-09-969-730-324
13	7	3.6	34	16	US-10-621-363-324
14	7	3.6	87	9	US-09-764-860-494
15	7	3.6	87	12	US-10-424-599-228701

16	7	3.6	87	14	US-10-074-095-494	Sequence 494, App
17	7	3.6	87	15	US-10-212-872-494	Sequence 494, App
18	7	3.6	110	10	US-09-847-208-65	Sequence 65, Appl
19	7	3.6	111	12	US-10-424-599-200520	Sequence 200520,
20	7	3.6	112	10	US-09-847-208-62	Sequence 62, Appl
21	7	3.6	124	14	US-10-156-761-8204	Sequence 8204, Ap
22	7	3.6	144	9	US-09-250-611-2	Sequence 2, Appli
23	7	3.6	176	14	US-10-321-856-73	Sequence 73, Appl
24	7	3.6	176	14	US-10-321-856-73	Sequence 73, Appl
25	7	3.6	191	9	US-09-733-507-2	Sequence 2, Appli
26	7	3.6	191	9	US-09-733-507-2	Sequence 10, Appl
27	7	3.6	204	9	US-09-250-611-4	Sequence 4, Appli
28	7	3.6	204	9	US-09-250-611-4	Sequence 9, Appli
29	7	3.6	210	12	US-10-282-122A-74257	Sequence 74257, A
30	7	3.6	224	9	US-09-925-300-1632	Sequence 1632, Ap
31	7	3.6	224	9	US-09-925-300-1632	Sequence 1632, A
32	7	3.6	260	14	US-10-369-493-16192	Sequence 11005, A
33	7	3.6	268	15	US-10-156-761-11005	Sequence 15441, A
34	7	3.6	268	15	US-10-369-493-15441	Sequence 15810, A
35	7	3.6	285	12	US-10-424-599-202185	Sequence 202185,
36	7	3.6	288	12	US-09-855-294B-3	Sequence 3, Appli
37	7	3.6	294	16	US-10-354-437-108	Sequence 108, App
38	7	3.6	296	15	US-10-369-493-9587	Sequence 9587, Ap
39	7	3.6	305	12	US-10-425-114-41813	Sequence 41813, A
40	7	3.6	327	12	US-10-282-122A-66710	Sequence 66710, A
41	7	3.6	327	12	US-10-072-012-34	Sequence 34, Appl
42	7	3.6	327	12	US-10-072-012-34	Sequence 342, App
43	7	3.6	359	12	US-10-206-576-472	Sequence 472, App
44	7	3.6	396	9	US-09-765-272-16	Sequence 16, Appl
45	7	3.6	405	12	US-10-424-599-168694	Sequence 168694,
46	7	3.6	419	10	US-09-769-787-157	Sequence 157, App
47	7	3.6	419	10	US-09-769-787-157	Sequence 74158, A
48	7	3.6	426	12	US-10-282-122A-74158	Sequence 40654, A
49	7	3.6	434	9	US-09-827-040-7	Sequence 7, Appli
50	7	3.6	434	13	US-10-060-425-15	Sequence 15, Appl
51	7	3.6	454	12	US-10-206-576-252	Sequence 252, App
52	7	3.6	476	9	US-09-827-040-3	Sequence 2, Appli
53	7	3.6	476	9	US-09-827-040-3	Sequence 3, Appli
54	7	3.6	476	9	US-09-827-040-6	Sequence 6, Appli
55	7	3.6	476	13	US-10-060-425-4	Sequence 4, Appli
56	7	3.6	476	13	US-10-060-425-12	Sequence 12, Appl
57	7	3.6	476	13	US-10-060-425-14	Sequence 14, Appl
58	7	3.6	476	15	US-10-395-027-576	Sequence 576, App
59	7	3.6	491	11	US-09-925-300-1715	Sequence 1715, Ap
60	7	3.6	491	11	US-09-833-245-1035	Sequence 1035, Ap
61	7	3.6	491	11	US-09-833-245-1057	Sequence 1057, Ap
62	7	3.6	557	15	US-10-369-493-159	Sequence 159, App
63	7	3.6	652	15	US-10-314-790-3	Sequence 3, Appli
64	7	3.6	816	15	US-10-369-493-18348	Sequence 18348, A
65	7	3.6	875	12	US-10-363-616-397	Sequence 397, App
66	7	3.6	894	12	US-10-206-576-248	Sequence 248, App
67	7	3.6	962	12	US-10-206-576-246	Sequence 246, App
68	7	3.6	962	12	US-10-206-576-250	Sequence 250, App
69	7	3.6	962	12	US-10-206-576-254	Sequence 254, App
70	7	3.6	962	12	US-10-206-576-470	Sequence 470, App
71	7	3.6	962	12	US-10-206-576-474	Sequence 474, App
72	7	3.6	962	12	US-10-206-576-478	Sequence 478, App
73	7	3.6	1083	15	US-10-369-493-21920	Sequence 21920, A
74	7	3.6	1203	15	US-10-320-797-3348	Sequence 3348, Ap
75	7	3.6	1209	14	US-10-032-585-7637	Sequence 7637, Ap
76	7	3.6	1242	9	US-09-925-299-911	Sequence 911, App
77	7	3.6	1242	10	US-09-925-299-911	Sequence 911, App
78	7	3.6	2515	12	US-10-042-865-53	Sequence 53, Appl
79	7	3.6	2515	12	US-10-029-020-53	Sequence 53, Appl
80	6	3.1	9	9	US-09-193-854-142	Sequence 142, App
81	6	3.1	9	9	US-09-968-561A-252	Sequence 252, App
82	6	3.1	9	10	US-09-968-744A-252	Sequence 252, App
83	6	3.1	9	12	US-09-968-561A-252	Sequence 252, App
84	6	3.1	9	14	US-10-353-929-114	Sequence 114, App
85	6	3.1	10	14	US-10-353-929-113	Sequence 113, App
86	6	3.1	15	10	US-09-984-271-200	Sequence 200, App
87	6	3.1	15	12	US-09-984-276-200	Sequence 200, App
88	6	3.1	16	10	US-09-965-536A-56	Sequence 56, Appl

89	6	3.1	16	10	US-09-984-271-201	Sequence 201, App	162	76	12	US-10-425-114-37848	Sequence 37848, A
90	6	3.1	16	12	US-09-984-276-201	Sequence 201, App	163	77	9	US-09-864-761-35634	Sequence 35634, A
91	6	3.1	20	9	US-09-864-761-40170	Sequence 40170, A	164	78	9	US-09-989-722-363	Sequence 363, App
92	6	3.1	25	9	US-09-864-761-46921	Sequence 46921, A	165	78	9	US-09-989-723-363	Sequence 363, App
93	6	3.1	25	10	US-09-933-767-823	Sequence 823, App	166	78	9	US-09-989-729-363	Sequence 363, App
94	6	3.1	29	10	US-09-933-767-1090	Sequence 1090, App	167	78	9	US-09-989-727-363	Sequence 363, App
95	6	3.1	29	12	US-10-004-860-823	Sequence 823, App	168	78	9	US-09-989-731-363	Sequence 363, App
96	6	3.1	29	12	US-10-004-860-1090	Sequence 1090, App	169	78	9	US-09-989-732-363	Sequence 363, App
97	6	3.1	29	14	US-10-023-282-823	Sequence 823, App	170	78	9	US-09-991-072-363	Sequence 363, App
98	6	3.1	29	14	US-10-023-282-1090	Sequence 1090, App	171	78	9	US-09-991-442-363	Sequence 363, App
99	6	3.1	32	9	US-09-864-761-39932	Sequence 39932, A	172	78	9	US-09-991-163-363	Sequence 363, App
100	6	3.1	32	9	US-09-828-708-73	Sequence 73, Appl	173	78	9	US-09-993-684-363	Sequence 363, App
101	6	3.1	32	10	US-09-965-536A-20	Sequence 20, Appl	174	78	9	US-09-990-456-363	Sequence 363, App
102	6	3.1	32	14	US-10-023-386-29209	Sequence 40553, A	175	78	9	US-09-992-598-363	Sequence 363, App
103	6	3.1	34	9	US-09-864-761-40553	Sequence 1022, App	176	78	9	US-09-989-721-363	Sequence 363, App
104	6	3.1	36	9	US-09-925-300-1022	Sequence 1022, App	177	78	9	US-09-992-598-363	Sequence 363, App
105	6	3.1	41	9	US-09-864-761-42758	Sequence 42758, A	178	78	9	US-09-993-296-15	Sequence 15, Appl
106	6	3.1	41	9	US-09-975-374A-18	Sequence 18, Appl	179	78	9	US-09-989-735-363	Sequence 363, App
107	6	3.1	41	14	US-10-144-929-228	Sequence 228, App	180	78	9	US-09-990-444-363	Sequence 363, App
108	6	3.1	41	15	US-10-144-929-238	Sequence 228, App	181	78	9	US-09-991-181-363	Sequence 363, App
109	6	3.1	44	10	US-09-764-891-3534	Sequence 3534, App	182	78	9	US-09-989-730-363	Sequence 363, App
110	6	3.1	46	9	US-09-738-626-4422	Sequence 4422, App	183	78	9	US-09-990-436-363	Sequence 363, App
111	6	3.1	46	15	US-10-375-932-130	Sequence 130, App	184	78	10	US-09-993-687-363	Sequence 363, App
112	6	3.1	46	15	US-10-375-932-131	Sequence 131, App	185	78	10	US-09-989-734-363	Sequence 363, App
113	6	3.1	46	15	US-10-375-932-132	Sequence 132, App	186	78	10	US-09-997-653-363	Sequence 363, App
114	6	3.1	47	12	US-10-424-599-202959	Sequence 202959, A	187	78	10	US-09-993-667-363	Sequence 363, App
115	6	3.1	47	12	US-10-424-599-266223	Sequence 266223, A	188	78	10	US-09-997-428-363	Sequence 363, App
116	6	3.1	48	14	US-10-424-599-26223	Sequence 26223, A	189	78	10	US-09-997-666-363	Sequence 363, App
117	6	3.1	51	11	US-09-864-408A-4080	Sequence 4080, App	190	78	10	US-09-990-438-363	Sequence 363, App
118	6	3.1	51	12	US-10-424-599-150848	Sequence 150848, A	191	78	10	US-09-990-562-363	Sequence 363, App
119	6	3.1	52	9	US-09-864-761-43582	Sequence 43582, A	192	78	10	US-09-990-711-363	Sequence 363, App
120	6	3.1	52	9	US-09-864-761-47325	Sequence 47325, A	193	78	10	US-09-989-726-363	Sequence 363, App
121	6	3.1	52	12	US-10-424-599-177066	Sequence 177066, A	194	78	10	US-09-998-156-363	Sequence 363, App
122	6	3.1	52	12	US-10-425-114-71273	Sequence 71273, A	195	78	10	US-09-990-437-363	Sequence 363, App
123	6	3.1	54	9	US-09-864-761-39215	Sequence 39215, A	196	78	10	US-09-991-157-363	Sequence 363, App
124	6	3.1	54	9	US-09-864-761-44300	Sequence 44300, A	197	78	10	US-09-997-514-363	Sequence 363, App
125	6	3.1	54	9	US-09-864-761-44300	Sequence 44300, A	198	78	10	US-09-997-573-363	Sequence 363, App
126	6	3.1	54	12	US-10-424-599-274266	Sequence 274266, A	199	78	10	US-09-991-172-363	Sequence 363, App
127	6	3.1	54	13	US-10-016-157A-193	Sequence 193, App	200	78	10	US-09-990-726-363	Sequence 363, App
128	6	3.1	54	14	US-10-219-329-7	Sequence 7, Appl	201	78	10	US-09-997-559-363	Sequence 363, App
129	6	3.1	54	14	US-10-153-185-7	Sequence 7, Appl	202	78	10	US-09-997-601-363	Sequence 363, App
130	6	3.1	54	14	US-10-219-561-7	Sequence 7, Appl	203	78	10	US-09-990-443-363	Sequence 363, App
131	6	3.1	55	9	US-09-764-855-138	Sequence 138, App	204	78	10	US-09-991-854-363	Sequence 363, App
132	6	3.1	55	12	US-10-424-599-169367	Sequence 169367, A	205	78	10	US-09-997-628-363	Sequence 363, App
133	6	3.1	55	12	US-10-424-599-284170	Sequence 284170, A	206	78	10	US-09-997-683-363	Sequence 363, App
134	6	3.1	55	14	US-10-072-349-138	Sequence 138, App	207	78	10	US-09-989-729A-363	Sequence 363, App
135	6	3.1	56	9	US-09-864-761-47236	Sequence 47236, A	208	78	10	US-09-997-349-363	Sequence 363, App
136	6	3.1	56	12	US-10-424-599-200649	Sequence 200649, A	209	78	10	US-09-997-440-363	Sequence 363, App
137	6	3.1	59	12	US-10-424-599-146489	Sequence 146489, A	210	78	10	US-09-990-440-363	Sequence 363, App
138	6	3.1	60	12	US-10-424-599-181547	Sequence 181547, A	211	78	10	US-09-993-469-363	Sequence 363, App
139	6	3.1	62	12	US-10-282-122A-49293	Sequence 49293, A	212	78	10	US-09-993-748-363	Sequence 363, App
140	6	3.1	62	12	US-10-424-599-163598	Sequence 163598, A	213	78	10	US-09-997-543-363	Sequence 363, App
141	6	3.1	64	9	US-09-864-761-35488	Sequence 35488, A	214	78	10	US-09-991-992-363	Sequence 363, App
142	6	3.1	64	9	US-09-864-761-45501	Sequence 45501, A	215	78	10	US-09-990-439-363	Sequence 363, App
143	6	3.1	64	12	US-10-424-599-242476	Sequence 242476, A	216	78	10	US-09-990-427-363	Sequence 363, App
144	6	3.1	67	14	US-10-106-698-5627	Sequence 5627, App	217	78	10	US-09-989-328-363	Sequence 363, App
145	6	3.1	68	12	US-10-424-599-153256	Sequence 153256, A	218	78	10	US-09-993-583-363	Sequence 363, App
146	6	3.1	68	12	US-10-424-599-245964	Sequence 245964, A	219	78	10	US-09-992-521-363	Sequence 363, App
147	6	3.1	70	10	US-09-813-153-100	Sequence 100, App	220	78	10	US-09-997-333-363	Sequence 363, App
148	6	3.1	71	12	US-10-424-599-181953	Sequence 181953, A	221	78	10	US-09-998-041-363	Sequence 363, App
149	6	3.1	71	12	US-10-424-599-225874	Sequence 225874, A	222	78	10	US-09-997-529-363	Sequence 363, App
150	6	3.1	72	12	US-10-424-599-180657	Sequence 180657, A	223	78	10	US-09-989-725-363	Sequence 363, App
151	6	3.1	73	12	US-10-424-599-242233	Sequence 242233, A	224	78	10	US-09-997-529-363	Sequence 363, App
152	6	3.1	73	12	US-10-424-599-267893	Sequence 267893, A	225	78	10	US-09-997-529-363	Sequence 363, App
153	6	3.1	74	9	US-09-925-302-509	Sequence 509, App	226	78	10	US-09-997-585-363	Sequence 363, App
154	6	3.1	74	9	US-09-864-761-35685	Sequence 35685, A	227	78	10	US-09-997-614-363	Sequence 363, App
155	6	3.1	74	12	US-09-925-302-509	Sequence 509, App	228	78	10	US-09-989-862-363	Sequence 363, App
156	6	3.1	75	9	US-09-864-761-40141	Sequence 40141, A	229	78	10	US-09-997-529-363	Sequence 363, App
157	6	3.1	75	15	US-10-264-049-3362	Sequence 3362, App	230	78	11	US-09-989-733-363	Sequence 363, App
158	6	3.1	76	12	US-10-424-599-153444	Sequence 153444, A	231	78	12	US-09-992-643-363	Sequence 242, App
159	6	3.1	76	12	US-10-424-599-170773	Sequence 170773, A	232	78	12	US-10-206-515-242	Sequence 242, App
160	6	3.1	76	12	US-10-424-599-200073	Sequence 200073, A	233	78	12	US-10-199-670-242	Sequence 242, App
161	6	3.1	76	12	US-10-424-599-275637	Sequence 275637, A	234	78	12	US-10-205-890-242	Sequence 242, App

235	6	3.1	78	12	US-10-201-853-242	Sequence 242, App	308	6	3.1	78	14	US-10-180-557-242	Sequence 242, App
236	6	3.1	78	12	US-10-063-745-363	Sequence 66, Appl	309	6	3.1	78	14	US-10-063-502-66	Sequence 66, Appl
237	6	3.1	78	12	US-09-989-724-363	Sequence 363, App	310	6	3.1	78	14	US-10-173-700-242	Sequence 242, App
238	6	3.1	78	12	US-09-989-728-363	Sequence 363, App	311	6	3.1	78	14	US-10-174-572-242	Sequence 242, App
239	6	3.1	78	12	US-09-990-441-363	Sequence 363, App	312	6	3.1	78	14	US-10-174-579-242	Sequence 242, App
240	6	3.1	78	12	US-10-063-512-66	Sequence 66, Appl	313	6	3.1	78	14	US-10-174-582-242	Sequence 242, App
241	6	3.1	78	12	US-10-063-513-66	Sequence 66, Appl	314	6	3.1	78	14	US-10-174-588-242	Sequence 242, App
242	6	3.1	78	12	US-10-063-515-66	Sequence 66, Appl	315	6	3.1	78	14	US-10-175-739-242	Sequence 242, App
243	6	3.1	78	12	US-10-063-549-66	Sequence 66, Appl	316	6	3.1	78	14	US-10-175-740-242	Sequence 242, App
244	6	3.1	78	12	US-10-063-569-66	Sequence 66, Appl	317	6	3.1	78	14	US-10-175-743-242	Sequence 242, App
245	6	3.1	78	12	US-10-063-551-66	Sequence 66, Appl	318	6	3.1	78	14	US-10-176-488-242	Sequence 242, App
246	6	3.1	78	12	US-10-174-581-242	Sequence 242, App	319	6	3.1	78	14	US-10-176-492-242	Sequence 242, App
247	6	3.1	78	12	US-10-176-483-242	Sequence 242, App	320	6	3.1	78	14	US-10-176-720-242	Sequence 242, App
248	6	3.1	78	12	US-10-176-749-242	Sequence 242, App	321	6	3.1	78	14	US-10-176-750-242	Sequence 242, App
249	6	3.1	78	12	US-10-176-914-242	Sequence 242, App	322	6	3.1	78	14	US-10-176-985-242	Sequence 242, App
250	6	3.1	78	12	US-10-176-915-242	Sequence 242, App	323	6	3.1	78	14	US-10-176-987-242	Sequence 242, App
251	6	3.1	78	12	US-09-997-857-363	Sequence 363, App	324	6	3.1	78	14	US-10-176-992-242	Sequence 242, App
252	6	3.1	78	12	US-10-063-555-66	Sequence 66, Appl	325	6	3.1	78	14	US-10-176-993-242	Sequence 242, App
253	6	3.1	78	12	US-10-063-563-66	Sequence 66, Appl	326	6	3.1	78	14	US-10-184-658-242	Sequence 242, App
254	6	3.1	78	12	US-10-063-594-66	Sequence 66, Appl	327	6	3.1	78	14	US-10-176-991-242	Sequence 242, App
255	6	3.1	78	12	US-10-063-553-66	Sequence 66, Appl	328	6	3.1	78	14	US-10-173-695-242	Sequence 242, App
256	6	3.1	78	12	US-10-063-554-66	Sequence 66, Appl	329	6	3.1	78	14	US-10-173-697-242	Sequence 242, App
257	6	3.1	78	12	US-10-176-484-242	Sequence 242, App	330	6	3.1	78	14	US-10-173-705-242	Sequence 242, App
258	6	3.1	78	12	US-10-180-550-242	Sequence 242, App	331	6	3.1	78	14	US-10-174-576-242	Sequence 242, App
259	6	3.1	78	12	US-10-183-014-242	Sequence 242, App	332	6	3.1	78	14	US-10-174-585-242	Sequence 242, App
260	6	3.1	78	12	US-10-187-738-242	Sequence 242, App	333	6	3.1	78	14	US-10-175-747-242	Sequence 242, App
261	6	3.1	78	12	US-10-187-740-242	Sequence 242, App	334	6	3.1	78	14	US-10-175-747-242	Sequence 242, App
262	6	3.1	78	12	US-10-187-883-242	Sequence 242, App	335	6	3.1	78	14	US-10-174-586-242	Sequence 242, App
263	6	3.1	78	12	US-10-194-363-242	Sequence 242, App	336	6	3.1	78	14	US-10-176-925-242	Sequence 242, App
264	6	3.1	78	12	US-10-194-460-242	Sequence 242, App	337	6	3.1	78	14	US-10-176-978-242	Sequence 242, App
265	6	3.1	78	12	US-10-194-463-242	Sequence 242, App	338	6	3.1	78	14	US-10-176-485-242	Sequence 242, App
266	6	3.1	78	12	US-10-194-484-242	Sequence 242, App	339	6	3.1	78	14	US-10-176-487-242	Sequence 242, App
267	6	3.1	78	12	US-10-195-884-242	Sequence 242, App	340	6	3.1	78	14	US-10-176-493-242	Sequence 242, App
268	6	3.1	78	12	US-10-195-896-242	Sequence 242, App	341	6	3.1	78	14	US-10-176-756-242	Sequence 242, App
269	6	3.1	78	12	US-10-196-744-242	Sequence 242, App	342	6	3.1	78	14	US-10-176-919-242	Sequence 242, App
270	6	3.1	78	12	US-10-196-755-242	Sequence 242, App	343	6	3.1	78	14	US-10-176-925-242	Sequence 242, App
271	6	3.1	78	12	US-10-196-757-242	Sequence 242, App	344	6	3.1	78	14	US-10-176-978-242	Sequence 242, App
272	6	3.1	78	12	US-10-197-704-242	Sequence 242, App	345	6	3.1	78	14	US-10-179-510-242	Sequence 242, App
273	6	3.1	78	12	US-10-197-710-242	Sequence 242, App	346	6	3.1	78	14	US-10-180-543-242	Sequence 242, App
274	6	3.1	78	12	US-10-198-758-242	Sequence 242, App	347	6	3.1	78	14	US-10-180-544-242	Sequence 242, App
275	6	3.1	78	12	US-10-198-766-242	Sequence 242, App	348	6	3.1	78	14	US-10-180-546-242	Sequence 242, App
276	6	3.1	78	12	US-10-199-304-242	Sequence 242, App	349	6	3.1	78	14	US-10-180-547-242	Sequence 242, App
277	6	3.1	78	12	US-10-199-309-242	Sequence 242, App	350	6	3.1	78	14	US-10-180-549-242	Sequence 242, App
278	6	3.1	78	12	US-10-199-313-242	Sequence 242, App	351	6	3.1	78	14	US-10-180-555-242	Sequence 242, App
279	6	3.1	78	12	US-10-199-456-242	Sequence 242, App	352	6	3.1	78	14	US-10-180-559-242	Sequence 242, App
280	6	3.1	78	12	US-10-201-329-242	Sequence 242, App	353	6	3.1	78	14	US-10-181-000-242	Sequence 242, App
281	6	3.1	78	12	US-10-202-412-242	Sequence 242, App	354	6	3.1	78	14	US-10-183-010-242	Sequence 242, App
282	6	3.1	78	12	US-10-206-919-242	Sequence 242, App	355	6	3.1	78	14	US-10-183-012-242	Sequence 242, App
283	6	3.1	78	12	US-10-206-922-242	Sequence 242, App	356	6	3.1	78	14	US-10-184-614-242	Sequence 242, App
284	6	3.1	78	12	US-10-206-924-242	Sequence 242, App	357	6	3.1	78	14	US-10-184-623-242	Sequence 242, App
285	6	3.1	78	12	US-10-206-928-242	Sequence 242, App	358	6	3.1	78	14	US-10-184-635-242	Sequence 242, App
286	6	3.1	78	12	US-10-207-314-242	Sequence 242, App	359	6	3.1	78	14	US-10-184-637-242	Sequence 242, App
287	6	3.1	78	12	US-10-207-921-242	Sequence 242, App	360	6	3.1	78	14	US-10-184-646-242	Sequence 242, App
288	6	3.1	78	12	US-10-207-922-242	Sequence 242, App	361	6	3.1	78	14	US-10-184-647-242	Sequence 242, App
289	6	3.1	78	12	US-10-208-027-242	Sequence 242, App	362	6	3.1	78	14	US-10-184-652-242	Sequence 242, App
290	6	3.1	78	12	US-09-997-641-363	Sequence 363, App	363	6	3.1	78	14	US-10-187-594-242	Sequence 242, App
291	6	3.1	78	12	US-09-991-150-363	Sequence 363, App	364	6	3.1	78	14	US-10-187-596-242	Sequence 242, App
292	6	3.1	78	12	US-10-174-570-242	Sequence 242, App	365	6	3.1	78	14	US-10-187-745-242	Sequence 242, App
293	6	3.1	78	12	US-10-183-005-242	Sequence 242, App	366	6	3.1	78	14	US-10-187-885-242	Sequence 242, App
294	6	3.1	78	12	US-10-006-867-66	Sequence 66, Appl	367	6	3.1	78	14	US-10-187-886-242	Sequence 242, App
295	6	3.1	78	12	US-10-063-547-66	Sequence 66, Appl	368	6	3.1	78	14	US-10-196-756-242	Sequence 242, App
296	6	3.1	78	12	US-10-174-590-242	Sequence 242, App	369	6	3.1	78	14	US-10-176-760-242	Sequence 242, App
297	6	3.1	78	12	US-10-176-758-242	Sequence 242, App	370	6	3.1	78	14	US-10-176-990-242	Sequence 242, App
298	6	3.1	78	12	US-10-175-737-242	Sequence 242, App	371	6	3.1	78	14	US-10-180-541-242	Sequence 242, App
299	6	3.1	78	12	US-10-173-706-242	Sequence 242, App	372	6	3.1	78	14	US-10-180-542-242	Sequence 242, App
300	6	3.1	78	12	US-10-173-706-66	Sequence 66, Appl	373	6	3.1	78	14	US-10-180-548-242	Sequence 242, App
301	6	3.1	78	12	US-10-173-738-242	Sequence 242, App	374	6	3.1	78	14	US-10-180-551-242	Sequence 242, App
302	6	3.1	78	12	US-10-175-738-242	Sequence 242, App	375	6	3.1	78	14	US-10-180-598-242	Sequence 242, App
303	6	3.1	78	12	US-10-175-752-242	Sequence 242, App	376	6	3.1	78	14	US-10-180-999-242	Sequence 242, App
304	6	3.1	78	12	US-10-176-482-242	Sequence 242, App	377	6	3.1	78	14	US-10-183-013-242	Sequence 242, App
305	6	3.1	78	12	US-10-176-757-242	Sequence 242, App	378	6	3.1	78	14	US-10-184-612-242	Sequence 242, App
306	6	3.1	78	12	US-10-176-913-242	Sequence 242, App	379	6	3.1	78	14	US-10-184-616-242	Sequence 242, App
307	6	3.1	78	12	US-10-180-552-242	Sequence 242, App	380	6	3.1	78	14	US-10-184-616-242	Sequence 242, App





6	3.1	78	14	US-10-199-318-242	Sequence 242, App	600	6	3.1	78	14	US-10-199-460-242	Sequence 242, App
6	3.1	78	14	US-10-199-458-242	Sequence 242, App	601	6	3.1	78	14	US-10-199-461-242	Sequence 242, App
6	3.1	78	14	US-10-199-462-242	Sequence 242, App	602	6	3.1	78	14	US-10-199-667-242	Sequence 242, App
6	3.1	78	14	US-10-201-324-242	Sequence 242, App	603	6	3.1	78	14	US-10-199-673-242	Sequence 242, App
6	3.1	78	14	US-10-201-328-242	Sequence 242, App	604	6	3.1	78	14	US-10-201-321-242	Sequence 242, App
6	3.1	78	14	US-10-201-328-242	Sequence 242, App	605	6	3.1	78	14	US-10-201-322-242	Sequence 242, App
6	3.1	78	14	US-10-201-528-242	Sequence 242, App	606	6	3.1	78	14	US-10-201-326-242	Sequence 242, App
6	3.1	78	14	US-10-201-529-242	Sequence 242, App	607	6	3.1	78	14	US-10-201-532-242	Sequence 242, App
6	3.1	78	14	US-10-201-530-242	Sequence 242, App	608	6	3.1	78	14	US-10-201-533-242	Sequence 242, App
6	3.1	78	14	US-10-202-408-242	Sequence 242, App	609	6	3.1	78	14	US-10-201-535-242	Sequence 242, App
6	3.1	78	14	US-10-202-409-242	Sequence 242, App	610	6	3.1	78	14	US-10-201-769-242	Sequence 242, App
6	3.1	78	14	US-10-202-411-242	Sequence 242, App	611	6	3.1	78	14	US-10-201-771-242	Sequence 242, App
6	3.1	78	14	US-10-202-472-242	Sequence 242, App	612	6	3.1	78	14	US-10-201-854-242	Sequence 242, App
6	3.1	78	14	US-10-202-472-242	Sequence 242, App	613	6	3.1	78	14	US-10-202-410-242	Sequence 242, App
6	3.1	78	14	US-10-205-502-242	Sequence 242, App	614	6	3.1	78	14	US-10-202-473-242	Sequence 242, App
6	3.1	78	14	US-10-205-502-242	Sequence 242, App	615	6	3.1	78	14	US-10-202-474-242	Sequence 242, App
6	3.1	78	14	US-10-205-511-242	Sequence 242, App	616	6	3.1	78	14	US-10-205-503-242	Sequence 242, App
6	3.1	78	14	US-10-205-907-242	Sequence 242, App	617	6	3.1	78	14	US-10-205-512-242	Sequence 242, App
6	3.1	78	14	US-10-205-907-242	Sequence 242, App	618	6	3.1	78	14	US-10-205-892-242	Sequence 242, App
6	3.1	78	14	US-10-194-456-242	Sequence 242, App	619	6	3.1	78	14	US-10-205-894-242	Sequence 242, App
6	3.1	78	14	US-10-196-758-242	Sequence 242, App	620	6	3.1	78	14	US-10-205-896-242	Sequence 242, App
6	3.1	78	14	US-10-198-770-242	Sequence 242, App	621	6	3.1	78	14	US-10-205-898-242	Sequence 242, App
6	3.1	78	14	US-10-199-308-242	Sequence 242, App	622	6	3.1	78	14	US-10-205-901-242	Sequence 242, App
6	3.1	78	14	US-10-200-617-242	Sequence 242, App	623	6	3.1	78	14	US-10-205-903-242	Sequence 242, App
6	3.1	78	14	US-10-205-893-242	Sequence 242, App	624	6	3.1	78	14	US-10-206-909-242	Sequence 242, App
6	3.1	78	14	US-10-205-897-242	Sequence 242, App	625	6	3.1	78	14	US-10-206-910-242	Sequence 242, App
6	3.1	78	14	US-10-196-754-242	Sequence 242, App	626	6	3.1	78	14	US-10-206-911-242	Sequence 242, App
6	3.1	78	14	US-10-174-571-242	Sequence 242, App	627	6	3.1	78	14	US-10-206-912-242	Sequence 242, App
6	3.1	78	14	US-10-176-746-242	Sequence 242, App	628	6	3.1	78	14	US-10-206-913-242	Sequence 242, App
6	3.1	78	14	US-10-176-923-242	Sequence 242, App	629	6	3.1	78	14	US-10-206-914-242	Sequence 242, App
6	3.1	78	14	US-10-183-011-242	Sequence 242, App	630	6	3.1	78	14	US-10-206-914-242	Sequence 242, App
6	3.1	78	14	US-10-184-633-242	Sequence 242, App	631	6	3.1	78	14	US-10-206-920-242	Sequence 242, App
6	3.1	78	14	US-10-184-639-242	Sequence 242, App	632	6	3.1	78	14	US-10-206-921-242	Sequence 242, App
6	3.1	78	14	US-10-187-742-242	Sequence 242, App	633	6	3.1	78	14	US-10-206-927-242	Sequence 242, App
6	3.1	78	14	US-10-187-748-242	Sequence 242, App	634	6	3.1	78	14	US-10-207-916-242	Sequence 242, App
6	3.1	78	14	US-10-188-766-561	Sequence 242, App	635	6	3.1	78	14	US-10-207-917-242	Sequence 242, App
6	3.1	78	14	US-10-188-771-242	Sequence 242, App	636	6	3.1	78	14	US-10-207-918-242	Sequence 242, App
6	3.1	78	14	US-10-192-006-242	Sequence 242, App	637	6	3.1	78	14	US-10-207-919-242	Sequence 242, App
6	3.1	78	14	US-10-192-008-242	Sequence 242, App	638	6	3.1	78	14	US-10-207-919-242	Sequence 242, App
6	3.1	78	14	US-10-192-009-242	Sequence 242, App	639	6	3.1	78	14	US-10-207-920-242	Sequence 242, App
6	3.1	78	14	US-10-192-012-242	Sequence 242, App	640	6	3.1	78	14	US-10-207-925-242	Sequence 242, App
6	3.1	78	14	US-10-192-012-242	Sequence 242, App	641	6	3.1	78	14	US-10-208-021-242	Sequence 242, App
6	3.1	78	14	US-10-192-016-242	Sequence 242, App	642	6	3.1	78	14	US-10-208-022-242	Sequence 242, App
6	3.1	78	14	US-10-194-362-242	Sequence 242, App	643	6	3.1	78	14	US-10-208-023-242	Sequence 242, App
6	3.1	78	14	US-10-194-364-242	Sequence 242, App	644	6	3.1	78	14	US-10-208-026-242	Sequence 242, App
6	3.1	78	14	US-10-194-395-242	Sequence 242, App	645	6	3.1	78	14	US-10-208-029-242	Sequence 242, App
6	3.1	78	14	US-10-194-424-242	Sequence 242, App	646	6	3.1	78	14	US-10-208-029-242	Sequence 242, App
6	3.1	78	14	US-10-194-458-242	Sequence 242, App	647	6	3.1	78	14	US-10-208-030-242	Sequence 242, App
6	3.1	78	14	US-10-194-459-242	Sequence 242, App	648	6	3.1	78	14	US-10-063-567-66	Sequence 66, Appl
6	3.1	78	14	US-10-194-488-242	Sequence 242, App	649	6	3.1	78	14	US-10-232-232-242	Sequence 242, App
6	3.1	78	14	US-10-195-886-242	Sequence 242, App	650	6	3.1	78	14	US-10-195-898-242	Sequence 242, App
6	3.1	78	14	US-10-195-891-242	Sequence 242, App	651	6	3.1	78	14	US-10-196-759-242	Sequence 242, App
6	3.1	78	14	US-10-196-746-242	Sequence 242, App	652	6	3.1	78	14	US-10-173-693-242	Sequence 242, App
6	3.1	78	14	US-10-196-752-242	Sequence 242, App	653	6	3.1	78	14	US-10-173-693-242	Sequence 242, App
6	3.1	78	14	US-10-196-753-242	Sequence 242, App	654	6	3.1	78	14	US-10-174-578-242	Sequence 242, App
6	3.1	78	14	US-10-196-753-242	Sequence 242, App	655	6	3.1	78	14	US-10-175-741-242	Sequence 242, App
6	3.1	78	14	US-10-197-693-242	Sequence 242, App	656	6	3.1	78	14	US-10-175-750-242	Sequence 242, App
6	3.1	78	14	US-10-197-696-242	Sequence 242, App	657	6	3.1	78	14	US-10-176-986-242	Sequence 242, App
6	3.1	78	14	US-10-197-698-242	Sequence 242, App	658	6	3.1	78	14	US-10-184-641-242	Sequence 242, App
6	3.1	78	14	US-10-197-703-242	Sequence 242, App	659	6	3.1	78	14	US-10-187-888-242	Sequence 242, App
6	3.1	78	14	US-10-197-711-242	Sequence 242, App	660	6	3.1	78	14	US-10-194-360-242	Sequence 242, App
6	3.1	78	14	US-10-198-757-242	Sequence 242, App	661	6	3.1	78	14	US-10-194-365-242	Sequence 242, App
6	3.1	78	14	US-10-198-761-242	Sequence 242, App	662	6	3.1	78	14	US-10-195-895-242	Sequence 242, App
6	3.1	78	14	US-10-198-762-242	Sequence 242, App	663	6	3.1	78	14	US-10-199-302-242	Sequence 242, App
6	3.1	78	14	US-10-198-763-242	Sequence 242, App	664	6	3.1	78	14	US-10-201-323-242	Sequence 242, App
6	3.1	78	14	US-10-198-767-242	Sequence 242, App	665	6	3.1	78	14	US-10-205-510-242	Sequence 242, App
6	3.1	78	14	US-10-198-767-242	Sequence 242, App	666	6	3.1	78	14	US-10-205-891-242	Sequence 242, App
6	3.1	78	14	US-10-199-301-242	Sequence 242, App	667	6	3.1	78	14	US-10-206-917-242	Sequence 242, App
6	3.1	78	14	US-10-199-307-242	Sequence 242, App	668	6	3.1	78	14	US-10-207-923-242	Sequence 242, App
6	3.1	78	14	US-10-199-312-242	Sequence 242, App	669	6	3.1	78	14	US-10-207-924-242	Sequence 242, App
6	3.1	78	14	US-10-199-315-242	Sequence 242, App	670	6	3.1	78	14	US-10-208-028-242	Sequence 242, App
6	3.1	78	14	US-10-199-316-242	Sequence 242, App	671	6	3.1	78	14	US-10-063-538-66	Sequence 66, Appl
6	3.1	78	14	US-10-199-457-242	Sequence 242, App	672	6	3.1	78	14	US-10-205-904-242	Sequence 242, App
6	3.1	78	14	US-10-199-459-242	Sequence 242, App	673	6	3.1	78	14	US-10-175-753-242	Sequence 242, App

673	6	3.1	78	14	US-10-180-553-242	Sequence 242, App	746
674	6	3.1	78	14	US-10-201-327-242	Sequence 242, App	747
675	6	3.1	78	14	US-10-121-062-242	Sequence 242, App	748
676	6	3.1	78	14	US-10-063-599-66	Sequence 66, Appl	749
677	6	3.1	78	14	US-10-183-003-242	Sequence 242, App	750
678	6	3.1	78	14	US-10-183-016-242	Sequence 242, App	751
679	6	3.1	78	14	US-10-173-696-242	Sequence 242, App	752
680	6	3.1	78	14	US-10-063-595-66	Sequence 66, Appl	753
681	6	3.1	78	14	US-10-125-923A-242	Sequence 242, App	754
682	6	3.1	78	14	US-10-176-491-242	Sequence 242, App	755
683	6	3.1	78	14	US-10-176-979-242	Sequence 242, App	756
684	6	3.1	78	14	US-10-187-592-242	Sequence 242, App	757
685	6	3.1	78	14	US-10-197-691-242	Sequence 242, App	758
686	6	3.1	78	14	US-10-198-771-242	Sequence 242, App	759
687	6	3.1	78	14	US-10-174-575A-242	Sequence 242, App	761
688	6	3.1	78	14	US-10-179-520-242	Sequence 242, App	762
689	6	3.1	78	14	US-10-201-325-242	Sequence 242, App	763
690	6	3.1	78	14	US-10-202-941-242	Sequence 242, App	764
691	6	3.1	78	14	US-10-205-910-242	Sequence 242, App	765
692	6	3.1	78	14	US-10-179-526-242	Sequence 242, App	766
693	6	3.1	78	14	US-10-173-701-242	Sequence 242, App	767
694	6	3.1	78	14	US-10-179-511-242	Sequence 242, App	768
695	6	3.1	78	14	US-10-179-518-242	Sequence 242, App	769
696	6	3.1	78	14	US-10-183-018-242	Sequence 242, App	770
697	6	3.1	78	14	US-10-184-624-242	Sequence 242, App	771
698	6	3.1	78	14	US-10-184-657-242	Sequence 242, App	772
699	6	3.1	78	14	US-10-197-706-242	Sequence 242, App	773
700	6	3.1	78	14	US-10-197-706-242	Sequence 242, App	774
701	6	3.1	78	14	US-10-201-857-242	Sequence 242, App	775
702	6	3.1	78	14	US-10-202-413-242	Sequence 242, App	776
703	6	3.1	78	14	US-10-202-938-242	Sequence 242, App	777
704	6	3.1	78	14	US-10-202-940-242	Sequence 242, App	778
705	6	3.1	78	14	US-10-205-508-242	Sequence 242, App	779
706	6	3.1	78	14	US-10-205-905-242	Sequence 242, App	780
707	6	3.1	78	14	US-10-206-918-242	Sequence 242, App	781
708	6	3.1	78	14	US-10-208-025-242	Sequence 242, App	782
709	6	3.1	78	14	US-10-063-580-66	Sequence 66, Appl	783
710	6	3.1	78	14	US-10-063-557-66	Sequence 66, Appl	784
711	6	3.1	78	14	US-10-198-760-242	Sequence 242, App	785
712	6	3.1	78	14	US-10-201-772-242	Sequence 242, App	786
713	6	3.1	78	14	US-10-063-585-66	Sequence 66, Appl	787
714	6	3.1	78	14	US-10-184-613-242	Sequence 242, App	788
715	6	3.1	78	14	US-10-187-739-242	Sequence 242, App	789
716	6	3.1	78	14	US-10-206-907-242	Sequence 242, App	790
717	6	3.1	78	14	US-10-183-009-242	Sequence 242, App	791
718	6	3.1	78	14	US-10-187-785-242	Sequence 66, Appl	792
719	6	3.1	78	14	US-10-063-588-66	Sequence 66, Appl	793
720	6	3.1	78	14	US-10-063-735-66	Sequence 66, Appl	794
721	6	3.1	78	14	US-10-199-672-242	Sequence 242, App	795
722	6	3.1	78	14	US-10-187-749-242	Sequence 242, App	796
723	6	3.1	78	14	US-10-194-457-242	Sequence 242, App	797
724	6	3.1	78	14	US-10-184-642-242	Sequence 242, App	798
725	6	3.1	78	14	US-10-196-747-242	Sequence 242, App	799
726	6	3.1	78	14	US-10-173-689-242	Sequence 242, App	800
727	6	3.1	78	14	US-10-173-690-242	Sequence 242, App	801
728	6	3.1	78	14	US-10-173-691-242	Sequence 242, App	802
729	6	3.1	78	14	US-10-173-692-242	Sequence 242, App	803
730	6	3.1	78	14	US-10-173-698-242	Sequence 242, App	804
731	6	3.1	78	14	US-10-173-699-242	Sequence 242, App	805
732	6	3.1	78	14	US-10-173-707-242	Sequence 242, App	806
733	6	3.1	78	14	US-10-174-569-242	Sequence 242, App	807
734	6	3.1	78	14	US-10-174-583-242	Sequence 242, App	808
735	6	3.1	78	14	US-10-174-587-242	Sequence 242, App	809
736	6	3.1	78	14	US-10-174-589-242	Sequence 242, App	810
737	6	3.1	78	14	US-10-174-591-242	Sequence 242, App	811
738	6	3.1	78	14	US-10-175-736-242	Sequence 242, App	812
739	6	3.1	78	14	US-10-175-742-242	Sequence 242, App	813
740	6	3.1	78	14	US-10-175-744-242	Sequence 242, App	814
741	6	3.1	78	14	US-10-175-745-242	Sequence 242, App	815
742	6	3.1	78	14	US-10-175-748-242	Sequence 242, App	816
743	6	3.1	78	14	US-10-175-751-242	Sequence 242, App	817
744	6	3.1	78	14	US-10-175-754-242	Sequence 242, App	818
745	6	3.1	78	14	US-10-176-480-242	Sequence 242, App	818
242, App					US-10-176-489-242	Sequence 242, App	
242, App					US-10-176-754-242	Sequence 242, App	
242, App					US-10-176-755-242	Sequence 242, App	
242, App					US-10-176-759-242	Sequence 242, App	
242, App					US-10-176-920-242	Sequence 242, App	
242, App					US-10-176-922-242	Sequence 242, App	
242, App					US-10-176-924-242	Sequence 242, App	
242, App					US-10-176-984-242	Sequence 242, App	
242, App					US-10-179-508-242	Sequence 242, App	
242, App					US-10-179-512-242	Sequence 242, App	
242, App					US-10-179-515-242	Sequence 242, App	
242, App					US-10-173-692-242	Sequence 242, App	
242, App					US-10-173-702-242	Sequence 242, App	
242, App					US-10-173-703-242	Sequence 242, App	
242, App					US-10-173-704-242	Sequence 242, App	
242, App					US-10-174-574-242	Sequence 242, App	
242, App					US-10-176-486-242	Sequence 242, App	
242, App					US-10-176-490-242	Sequence 242, App	
242, App					US-10-176-752-242	Sequence 242, App	
242, App					US-10-176-981-242	Sequence 242, App	
242, App					US-10-176-983-242	Sequence 242, App	
242, App					US-10-176-988-242	Sequence 242, App	
242, App					US-10-179-517-242	Sequence 242, App	
242, App					US-10-179-521-242	Sequence 242, App	
242, App					US-10-063-526-66	Sequence 66, Appl	
242, App					US-10-063-586-66	Sequence 66, Appl	
242, App					US-10-063-586-66	Sequence 66, Appl	
242, App					US-10-063-564-66	Sequence 66, Appl	
242, App					US-10-063-662-66	Sequence 66, Appl	
242, App					US-10-063-510-66	Sequence 66, Appl	
242, App					US-10-063-669-66	Sequence 66, Appl	
242, App					US-10-063-670-66	Sequence 66, Appl	
242, App					US-10-063-671-66	Sequence 66, Appl	
242, App					US-10-063-674-66	Sequence 66, Appl	
242, App					US-10-063-675-66	Sequence 66, Appl	
242, App					US-10-063-676-66	Sequence 66, Appl	
242, App					US-10-063-686-66	Sequence 66, Appl	
242, App					US-10-063-689-66	Sequence 66, Appl	
242, App					US-10-063-692-66	Sequence 66, Appl	
242, App					US-10-063-693-66	Sequence 66, Appl	
242, App					US-10-063-694-66	Sequence 66, Appl	
242, App					US-10-063-698-66	Sequence 66, Appl	
242, App					US-10-063-699-66	Sequence 66, Appl	
242, App					US-10-063-702-66	Sequence 66, Appl	
242, App					US-10-063-705-66	Sequence 66, Appl	
242, App					US-10-063-707-66	Sequence 66, Appl	
242, App					US-10-063-709-66	Sequence 66, Appl	
242, App					US-10-063-713-66	Sequence 66, Appl	
242, App					US-10-063-724-66	Sequence 66, Appl	
242, App					US-10-063-727-66	Sequence 66, Appl	
242, App					US-10-063-730-66	Sequence 66, Appl	
242, App					US-10-063-734-66	Sequence 66, Appl	
242, App					US-10-063-736-66	Sequence 66, Appl	
242, App					US-10-063-742-66	Sequence 66, Appl	
242, App					US-10-063-743-66	Sequence 66, Appl	
242, App					US-10-063-744-66	Sequence 66, Appl	
242, App					US-10-202-475-242	Sequence 242, App	
242, App					US-10-063-565-66	Sequence 66, Appl	
242, App					US-10-063-577-66	Sequence 66, Appl	
242, App					US-10-063-591-66	Sequence 66, Appl	
242, App					US-10-063-610-66	Sequence 66, Appl	
242, App					US-10-063-673-66	Sequence 66, Appl	
242, App					US-10-063-710-66	Sequence 66, Appl	
242, App					US-10-063-711-66	Sequence 66, Appl	
242, App					US-10-063-712-66	Sequence 66, Appl	
242, App					US-10-063-714-66	Sequence 66, Appl	
242, App					US-10-063-715-66	Sequence 66, Appl	
242, App					US-10-063-716-66	Sequence 66, Appl	
242, App					US-10-063-717-66	Sequence 66, Appl	
242, App					US-10-063-720-66	Sequence 66, Appl	
242, App					US-10-063-722-66	Sequence 66, Appl	
242, App					US-10-063-726-66	Sequence 66, Appl	
242, App					US-10-063-728-66	Sequence 66, Appl	

819	6	3.1	78	14	US-10-063-731-66	Sequence 66, Appl	892	6	3.1	78	15	US-10-195-887-242	Sequence 242, App
820	6	3.1	78	14	US-10-063-732-66	Sequence 66, Appl	893	6	3.1	78	15	US-10-195-893-242	Sequence 242, App
821	6	3.1	78	14	US-10-063-523-66	Sequence 66, Appl	894	6	3.1	78	15	US-10-179-509-242	Sequence 242, App
822	6	3.1	78	14	US-10-063-527-66	Sequence 66, Appl	895	6	3.1	78	15	US-10-194-486-242	Sequence 242, App
823	6	3.1	78	14	US-10-063-529-66	Sequence 66, Appl	896	6	3.1	78	15	US-10-195-900-242	Sequence 242, App
824	6	3.1	78	14	US-10-063-581-66	Sequence 66, Appl	897	6	3.1	78	15	US-10-198-759-242	Sequence 242, App
825	6	3.1	78	14	US-10-063-583-66	Sequence 66, Appl	898	6	3.1	78	15	US-10-205-506-242	Sequence 242, App
826	6	3.1	78	14	US-10-063-589-66	Sequence 66, Appl	899	6	3.1	78	15	US-10-199-523-242	Sequence 242, App
827	6	3.1	78	14	US-10-063-593-66	Sequence 66, Appl	900	6	3.1	78	15	US-10-199-463-242	Sequence 242, App
828	6	3.1	78	14	US-10-063-598-66	Sequence 66, Appl	901	6	3.1	78	15	US-10-202-471-242	Sequence 242, App
829	6	3.1	78	14	US-10-063-600-66	Sequence 66, Appl	902	6	3.1	78	15	US-10-207-915-242	Sequence 242, App
830	6	3.1	78	14	US-10-063-604-66	Sequence 66, Appl	903	6	3.1	78	15	US-10-213-538-363	Sequence 363, App
831	6	3.1	78	14	US-10-063-607-66	Sequence 66, Appl	904	6	3.1	78	16	US-10-197-709-242	Sequence 242, App
832	6	3.1	78	14	US-10-063-612-66	Sequence 66, Appl	905	6	3.1	80	9	US-09-864-761-35659	Sequence 35659, A
833	6	3.1	78	14	US-10-063-615-66	Sequence 66, Appl	906	6	3.1	81	12	US-10-424-599-216251	Sequence 216251, A
834	6	3.1	78	14	US-10-063-640-66	Sequence 66, Appl	907	6	3.1	82	12	US-10-424-599-252118	Sequence 252118, A
835	6	3.1	78	14	US-10-063-642-66	Sequence 66, Appl	908	6	3.1	85	12	US-10-424-599-259594	Sequence 259594, A
836	6	3.1	78	14	US-10-063-644-66	Sequence 66, Appl	909	6	3.1	85	12	US-09-864-761-39399	Sequence 39399, A
837	6	3.1	78	14	US-10-063-649-66	Sequence 66, Appl	910	6	3.1	85	12	US-10-424-599-190825	Sequence 190825, A
838	6	3.1	78	14	US-10-063-650-66	Sequence 66, Appl	911	6	3.1	86	9	US-09-864-761-39192	Sequence 39192, A
839	6	3.1	78	14	US-10-063-652-66	Sequence 66, Appl	912	6	3.1	86	11	US-09-864-408A-7192	Sequence 7192, A
840	6	3.1	78	14	US-10-063-654-66	Sequence 66, Appl	913	6	3.1	86	11	US-09-833-245-868	Sequence 868, App
841	6	3.1	78	14	US-10-063-659-66	Sequence 66, Appl	914	6	3.1	87	9	US-09-864-761-39625	Sequence 39625, A
842	6	3.1	78	14	US-10-063-661-66	Sequence 66, Appl	915	6	3.1	87	9	US-09-864-761-45003	Sequence 45003, A
843	6	3.1	78	14	US-10-063-528-66	Sequence 66, Appl	916	6	3.1	87	12	US-10-351-334-326	Sequence 326, App
844	6	3.1	78	14	US-10-063-540-66	Sequence 66, Appl	917	6	3.1	88	12	US-10-424-599-179331	Sequence 179331, A
845	6	3.1	78	14	US-10-063-568-66	Sequence 66, Appl	918	6	3.1	89	12	US-09-864-761-44120	Sequence 44120, A
846	6	3.1	78	14	US-10-063-570-66	Sequence 66, Appl	919	6	3.1	89	12	US-09-764-856-49	Sequence 49, Appl
847	6	3.1	78	14	US-10-063-582-66	Sequence 66, Appl	920	6	3.1	91	9	US-10-102-627-49	Sequence 49, Appl
848	6	3.1	78	14	US-10-063-587-66	Sequence 66, Appl	921	6	3.1	91	9	US-09-864-761-34175	Sequence 34175, A
849	6	3.1	78	14	US-10-063-592-66	Sequence 66, Appl	922	6	3.1	92	9	US-09-893-737-204	Sequence 204, App
850	6	3.1	78	14	US-10-063-597-66	Sequence 66, Appl	923	6	3.1	92	14	US-10-137-765-51	Sequence 51, Appl
851	6	3.1	78	14	US-10-063-602-66	Sequence 66, Appl	924	6	3.1	92	14	US-10-146-337-51	Sequence 51, Appl
852	6	3.1	78	14	US-10-063-606-66	Sequence 66, Appl	925	6	3.1	93	12	US-10-424-599-146730	Sequence 146730, A
853	6	3.1	78	14	US-10-063-609-66	Sequence 66, Appl	926	6	3.1	93	12	US-10-424-599-273539	Sequence 273539, A
854	6	3.1	78	14	US-10-063-611-66	Sequence 66, Appl	927	6	3.1	96	14	US-10-156-761-8079	Sequence 8079, App
855	6	3.1	78	14	US-10-063-614-66	Sequence 66, Appl	928	6	3.1	97	12	US-10-424-599-223887	Sequence 223887, A
856	6	3.1	78	14	US-10-063-639-66	Sequence 66, Appl	929	6	3.1	97	12	US-10-425-114-56699	Sequence 56699, A
857	6	3.1	78	14	US-10-063-643-66	Sequence 66, Appl	930	6	3.1	97	12	US-09-925-298-604	Sequence 604, App
858	6	3.1	78	14	US-10-063-646-66	Sequence 66, Appl	931	6	3.1	97	14	US-10-102-806-604	Sequence 604, App
859	6	3.1	78	14	US-10-063-651-66	Sequence 66, Appl	932	6	3.1	97	15	US-10-264-049-2757	Sequence 2757, App
860	6	3.1	78	14	US-10-063-653-66	Sequence 66, Appl	933	6	3.1	98	9	US-09-205-658-58	Sequence 58, Appl
861	6	3.1	78	14	US-10-063-660-66	Sequence 66, Appl	934	6	3.1	98	9	US-09-844-353A-58	Sequence 58, Appl
862	6	3.1	78	14	US-10-063-665-66	Sequence 66, Appl	935	6	3.1	98	9	US-09-864-761-40415	Sequence 40415, A
863	6	3.1	78	14	US-10-063-684-66	Sequence 66, Appl	936	6	3.1	98	10	US-09-963-693-58	Sequence 58, Appl
864	6	3.1	78	14	US-10-063-536-66	Sequence 66, Appl	937	6	3.1	98	12	US-10-424-599-245153	Sequence 245153, A
865	6	3.1	78	14	US-10-063-562-66	Sequence 66, Appl	938	6	3.1	98	12	US-10-425-114-52612	Sequence 52612, A
866	6	3.1	78	14	US-10-063-638-66	Sequence 66, Appl	939	6	3.1	99	9	US-09-864-761-38013	Sequence 38013, A
867	6	3.1	78	14	US-10-063-638-66	Sequence 66, Appl	940	6	3.1	99	9	US-09-864-761-42990	Sequence 42990, A
868	6	3.1	78	14	US-10-063-666-66	Sequence 66, Appl	941	6	3.1	99	14	US-10-029-386-27410	Sequence 27410, A
869	6	3.1	78	14	US-10-063-672-66	Sequence 66, Appl	942	6	3.1	100	12	US-10-425-114-62186	Sequence 62186, A
870	6	3.1	78	14	US-10-063-721-66	Sequence 66, Appl	943	6	3.1	101	12	US-10-276-774-1655	Sequence 1655, App
871	6	3.1	78	14	US-10-063-723-66	Sequence 66, Appl	944	6	3.1	102	12	US-10-424-599-247392	Sequence 247392, A
872	6	3.1	78	14	US-10-063-514-66	Sequence 66, Appl	945	6	3.1	103	12	US-10-424-599-242138	Sequence 242138, A
873	6	3.1	78	14	US-10-063-516-66	Sequence 66, Appl	946	6	3.1	103	12	US-10-369-493-23002	Sequence 23002, A
874	6	3.1	78	14	US-10-063-529-66	Sequence 66, Appl	947	6	3.1	104	12	US-10-335-977-5013	Sequence 5013, App
875	6	3.1	78	14	US-10-063-684-66	Sequence 66, Appl	948	6	3.1	105	12	US-10-424-599-232000	Sequence 232000, A
876	6	3.1	78	14	US-10-063-688-66	Sequence 66, Appl	949	6	3.1	105	14	US-10-029-386-30635	Sequence 30635, A
877	6	3.1	78	14	US-10-063-520-66	Sequence 66, Appl	950	6	3.1	106	9	US-09-739-438-6	Sequence 6, Appl
878	6	3.1	78	14	US-10-063-647-66	Sequence 66, Appl	951	6	3.1	106	12	US-10-424-599-206052	Sequence 206052, A
879	6	3.1	78	14	US-10-063-548-66	Sequence 66, Appl	952	6	3.1	106	12	US-10-104-047-3270	Sequence 3270, App
880	6	3.1	78	14	US-10-063-578-66	Sequence 66, Appl	953	6	3.1	107	12	US-10-424-599-211471	Sequence 211471, A
881	6	3.1	78	14	US-10-063-648-66	Sequence 66, Appl	954	6	3.1	107	15	US-10-630-590-150	Sequence 150, App
882	6	3.1	78	14	US-10-063-677-66	Sequence 66, Appl	955	6	3.1	108	16	US-10-425-563-20	Sequence 20, Appl
883	6	3.1	78	14	US-10-063-718-66	Sequence 66, Appl	956	6	3.1	110	10	US-09-847-208-12	Sequence 12, Appl
884	6	3.1	78	14	US-10-063-741-66	Sequence 66, Appl	957	6	3.1	110	12	US-10-282-1228-69197	Sequence 69197, A
885	6	3.1	78	14	US-10-063-617-66	Sequence 66, Appl	958	6	3.1	111	10	US-09-847-208-60	Sequence 60, Appl
886	6	3.1	78	14	US-10-063-664-66	Sequence 66, Appl	959	6	3.1	111	12	US-10-282-1228-55306	Sequence 55306, A
887	6	3.1	78	14	US-10-063-561-66	Sequence 66, Appl	960	6	3.1	111	12	US-10-424-599-181954	Sequence 181954, A
888	6	3.1	78	14	US-10-063-618-66	Sequence 66, Appl	961	6	3.1	111	14	US-10-230-331-30	Sequence 30, Appl
889	6	3.1	78	14	US-10-063-657-66	Sequence 66, Appl	962	6	3.1	113	10	US-09-847-208-9	Sequence 9, Appl
890	6	3.1	78	14	US-10-063-668-66	Sequence 66, Appl	963	6	3.1	113	12	US-10-424-599-244539	Sequence 244539, A
891	6	3.1	78	15	US-10-063-550-66	Sequence 66, Appl	964	6	3.1	113	14	US-10-230-331-31	Sequence 31, Appl



PRIOR APPLICATION NUMBER: US 60/064,900  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,988  
PRIOR FILING DATE: 1997-11-07  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 611  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 145  
LENGTH: 194

TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (138)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-621-401-145

Query Match 99.5%; Score 193; DB 12; Length 194;  
Best Local Similarity 100.0%; Pred. No. 2.3e-180;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLRGSGFESVNSYFDSFLELLGK 60  
DB 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLRGSGFESVNSYFDSFLELLGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXISCSLKLKSLGFSVSKVEACDSLVDVTFTVNTLGCRRPFMSQ 180  
DB 121 TCGANKYRCDAKFRWCLXISCSLKLKSLGFSVSKVEACDSLVDVTFTVNTLGCRRPFMSQ 180

QY 181 RAACICAEKEEEL 194  
DB 181 RAACICAEKEEEL 194

## RESULT 3

US-09-305-736-144  
Sequence 144, Application US/09305736  
Publication No. US20030088078A1  
GENERAL INFORMATION:

APPLICANT: Feng et al.  
TITLE OF INVENTION: 125 Human Secreted Proteins  
FILE REFERENCE: P2020P1  
CURRENT APPLICATION NUMBER: US/09/305,736  
CURRENT FILING DATE: 1999-05-05  
EARLIER APPLICATION NUMBER: PCT/US98/23435  
EARLIER FILING DATE: 1998-11-04  
EARLIER APPLICATION NUMBER: 60/064,911  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,912  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,983  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,900  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,988  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,987  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,908  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,984  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,985  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/066,094  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,100  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,089

EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,095  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,090  
EARLIER FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 612  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 144  
LENGTH: 195  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (138)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (195)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-305-736-144

Query Match 99.5%; Score 193; DB 10; Length 195;  
Best Local Similarity 100.0%; Pred. No. 2.3e-180;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLRGSGFESVNSYFDSFLELLGK 60  
DB 1 MKLASGFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHLRGSGFESVNSYFDSFLELLGK 60  
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCLXISCSLKLKSLGFSVSKVEACDSLVDVTFTVNTLGCRRPFMSQ 180  
DB 121 TCGANKYRCDAKFRWCLXISCSLKLKSLGFSVSKVEACDSLVDVTFTVNTLGCRRPFMSQ 180  
QY 181 RAACICAEKEEEL 194  
DB 181 RAACICAEKEEEL 194

## RESULT 4

US-09-818-683-144  
Sequence 144, Application US/09818683  
Publication No. US20030211472A1  
GENERAL INFORMATION:

APPLICANT: Feng et al.  
TITLE OF INVENTION: 125 Human Secreted Proteins  
FILE REFERENCE: P2020P1  
CURRENT APPLICATION NUMBER: US/09/818,683  
CURRENT FILING DATE: 2001-03-28  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 612  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 144  
LENGTH: 195  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (138)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (195)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-818-683-144

Query Match 99.5%; Score 193; DB 11; Length 195;  
Best Local Similarity 100.0%; Pred. No. 2.3e-180;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon May 17 11:51:01 2004

Y 1 MKLASGFLVLSLGGGAGSDTSPDTEESYSDWGLRHRLRGSPESVNSYFDSFLELLGGK 60  
b 1 MKLASGFLVLSLGGGAGSDTSPDTEESYSDWGLRHRLRGSPESVNSYFDSFLELLGGK 60  
Y 61 NGVCQYRCRYGKAPMPRGYKQPGNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120  
b 61 NGVCQYRCRYGKAPMPRGYKQPGNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120  
Y 121 TCGANKYRCDAKPRWCLXISCDLKRSLGFSYKVEACDLSLVDVTWTLGCRPFMNSQ 180  
b 121 TCGANKYRCDAKPRWCLXISCDLKRSLGFSYKVEACDLSLVDVTWTLGCRPFMNSQ 180  
Y 181 RAACICABEEKEEL 194  
b 181 RAACICABEEKEEL 194

RESULT 5  
US-10-363-616-357  
; Sequence 357, Application US/10363616  
; Publication No. US20040044181A1  
; GENERAL INFORMATION:  
; APPLICANT: Hysag, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-113 (793)  
; CURRENT APPLICATION NUMBER: US/10/363,616  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 09/654,935  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 490  
; SEQ ID NO 357  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-363-616-357

Query Match 70.6%; Score 137; DB 12; Length 194;  
Best Local Similarity 100.0%; Pred. No. 1.3e-125;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 MKLASGFLVLSLGGGAGSDTSPDTEESYSDWGLRHRLRGSPESVNSYFDSFLELLGGK 60  
b 1 MKLASGFLVLSLGGGAGSDTSPDTEESYSDWGLRHRLRGSPESVNSYFDSFLELLGGK 60  
Y 61 NGVCQYRCRYGKAPMPRGYKQPGNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120  
b 61 NGVCQYRCRYGKAPMPRGYKQPGNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120  
Y 121 TCGANKYRCDAKPRWCL 137  
b 121 TCGANKYRCDAKPRWCL 137

RESULT 6  
US-09-975-374A-13  
; Sequence 13, Application US/09975374A  
; Patent No. US20020119139A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LAMBEAU, GERARD  
; APPLICANT: VALENTIN, EMMANUEL  
; TITLE OF INVENTION: CLONING AND RECOMBINANT EXPRESSION OF MAMMALIAN GROUP  
; TITLE OF INVENTION: X11 SECRETED PHOSPHOLIPASE A2  
; FILE REFERENCE: 1479-R-00  
; CURRENT APPLICATION NUMBER: US/09/975,374A  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: 60/239,489  
; PRIOR FILING DATE: 2000-10-11  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 194  
; TYPE: PRT

; ORGANISM: Xenopus sp.  
US-09-975-374A-13  
Query Match 4.1%; Score 8; DB 9; Length 194;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 179 SQAACIC 186  
b 179 SQAACIC 186

RESULT 7  
US-10-425-114-45178  
; Sequence 45178, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 45178  
; LENGTH: 306  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700455612\_FLI.pap  
US-10-425-114-45178

Query Match 4.1%; Score 8; DB 12; Length 306;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 187 ABEKEEL 194  
b 227 ABEKEEL 234

RESULT 8  
US-10-156-761-13394  
; Sequence 13394, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 13394  
; LENGTH: 484  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-13394



us-10-621-401-145.oligo.rapb

Mon May 17 11:51:01 2004

Query Match 4.1%; Score 8; DB 14; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SLGGGLAQ 20  
 DB 105 SLGGGLAQ 112

RESULT 9  
 US-10-425-114-51651  
 ; Sequence 51651, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaska, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 51651  
 ; LENGTH: 679  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700083042\_FLI.pep  
 US-10-425-114-51651

Query Match 4.1%; Score 8; DB 12; Length 679;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEEL 194  
 DB 600 ABEKEEL 607

RESULT 10  
 US-10-425-114-56183  
 ; Sequence 56183, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaska, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 56183  
 ; LENGTH: 780  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700210018\_FLI.pep  
 US-10-425-114-56183

Query Match 4.1%; Score 8; DB 12; Length 780;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEEL 194

Db 701 ABEKEEL 708

RESULT 11  
 US-09-774-639-334  
 ; Sequence 334, Application US/09774639  
 ; Publication No. US20030003555A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 90 Human Secreted Proteins  
 ; FILE REFERENCE: PZ013P1  
 ; CURRENT APPLICATION NUMBER: US/09/774,639  
 ; CURRENT FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 371  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 334  
 ; LENGTH: 34  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; ORGANISM: Homo sapiens  
 US-09-774-639-334

Query Match 3.6%; Score 7; DB 10; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LWSLGG 16  
 DB 2 LWSLGG 8

RESULT 12  
 US-09-969-730-324  
 ; Sequence 324, Application US/09969730  
 ; Publication No. US20030054443A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: 90 Human Secreted Proteins  
 ; FILE REFERENCE: PZ013P2  
 ; CURRENT APPLICATION NUMBER: US/09/969,730  
 ; CURRENT FILING DATE: 2001-10-04  
 ; PRIOR APPLICATION NUMBER: 09/774,639  
 ; PRIOR FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: 60/238,291  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 09/244,112  
 ; PRIOR FILING DATE: 1999-02-04  
 ; PRIOR APPLICATION NUMBER: PCT/US98/16235  
 ; PRIOR FILING DATE: 1998-08-04  
 ; PRIOR APPLICATION NUMBER: 60/056,371  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,732  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,366  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,364  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,370  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,367  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,365  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,731  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,557  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/056,563  
 ; PRIOR FILING DATE: 1997-08-19  
 ; PRIOR APPLICATION NUMBER: 60/055,970  
 ; PRIOR FILING DATE: 1997-08-18



Mon May 17 11:51:01 2004

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 373  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 324  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-621-363-324

Query Match 3.6%; Score 7; DB 16; Length 34;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LWLSLGG 16  
Db 2 LWLSLGG 8

RESULT 14

US-09-764-860-494  
; Sequence 494, Application US/09764860  
; Patent No. US20020094953A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008  
; CURRENT APPLICATION NUMBER: US/09/764,860  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 494  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-860-494

Query Match 3.6%; Score 7; DB 9; Length 87;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LVLWLSL 14  
Db 42 LVLWLSL 49

RESULT 15

US-10-424-599-228701  
; Sequence 228701, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 228701  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_48544C.1.pep  
US-10-424-599-228701

Query Match 3.6%; Score 7; DB 12; Length 87;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: 60/055,986  
PRIOR FILING DATE: 1997-08-18  
PRIOR APPLICATION NUMBER: 60/055,311  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,808  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,803  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,804  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,809  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,806  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,310  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,798  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,309  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,312  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,807  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,386  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,373  
; NUMBER OF SEQ ID NOS: 373  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 324  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-969-730-324

Query Match 3.6%; Score 7; DB 10; Length 34;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LWLSLGG 16  
Db 2 LWLSLGG 8

RESULT 13

US-10-621-363-324  
; Sequence 324, Application US/10621363  
; Publication No. US20040023283A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: PZ0132C1  
; CURRENT APPLICATION NUMBER: US/10/621,363  
; CURRENT FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: 09/969,730  
; PRIOR FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: 09/774,639  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/238,291  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 09/244,112  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: PCT/US98/16235  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/056,371  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,732  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,366  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,364  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,370  
; PRIOR FILING DATE: 1997-08-19

us-10-621-401-145.oligo.rapb

Mon May 17 11:51:01 2004

OY 47 NSYFDSF 53  
| | | | |  
Db 51 NSYFDSF 57

Search completed: May 17, 2004, 10:58:50  
Job time : 80 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:48:45 ; Search time 20 Seconds  
(without alignments)  
933.058 Million cell updates/sec

Title: US-10-621-401-145  
Perfect score: 194  
Sequence: 1 MKLASGLVWLGLGGLAQ.....PFMNSQRAACICAEERKEEL 194

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR\_78:\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	4.1	214	1	W2AD41	late I3 23K protei
2	8	4.1	528	2	B96545	hypothetical prote
3	8	4.1	637	2	T39291	hypothetical C242
4	8	4.1	768	2	C96545	hypothetical prote
5	7	3.6	63	2	A12413	hypothetical prote
6	7	3.6	75	2	C90225	hypothetical prote
7	7	3.6	75	2	C90342	hypothetical prote
8	7	3.6	106	1	R5BY1B	acidic ribosomal p
9	7	3.6	106	1	R5BY2B	acidic ribosomal p
10	7	3.6	106	2	T52147	ribosomal protein
11	7	3.6	110	1	R5BYA1	acidic ribosomal p
12	7	3.6	111	2	S43115	acidic ribosomal p
13	7	3.6	191	2	T01132	cyclin-dependent k
14	7	3.6	255	2	S34144	lipase - Serratia
15	7	3.6	298	2	T29685	hypothetical prote
16	7	3.6	317	2	A97684	hypothetical prote
17	7	3.6	317	2	AB2909	rhizobioicin (impor
18	7	3.6	319	2	S32923	phospholipase A1 (
19	7	3.6	320	2	AB0330	phospholipase A (i
20	7	3.6	327	2	G83058	probable permease
21	7	3.6	343	2	E64363	acidic ribosomal p
22	7	3.6	418	2	T01021	hypothetical prote
23	7	3.6	419	2	G95221	sugar ABC transpor
24	7	3.6	419	2	F98085	hypothetical prote
25	7	3.6	420	2	B42400	sugar-binding prot
26	7	3.6	448	2	F83724	Na+-transporting A
27	7	3.6	448	2	A24327	carboxypeptidase E
28	7	3.6	451	2	G70241	hypothetical prote
29	7	3.6	464	2	G71082	probable mannose-1

30	7	3.6	465	2	G75104	mannose-6-phosphat
31	7	3.6	476	2	S12461	carboxypeptidase E
32	7	3.6	476	2	A40469	carboxypeptidase E
33	7	3.6	476	2	S09489	carboxypeptidase E
34	7	3.6	477	2	S16383	carboxypeptidase E
35	7	3.6	519	2	H96661	unknown protein, 5
36	7	3.6	557	2	A70480	carbamoyl-phosphat
37	7	3.6	585	2	S69216	sulfur deprivation
38	7	3.6	632	2	F96544	hypothetical prote
39	7	3.6	652	2	A37000	leukemia virus rec
40	7	3.6	677	2	F83954	flagella-associate
41	7	3.6	736	2	T00313	catalase (EC 1.11.
42	7	3.6	780	2	F98840	hypothetical prote
43	7	3.6	783	2	B98602	hypothetical prote
44	7	3.6	791	2	T12455	hypothetical prote
45	7	3.6	812	2	H96544	ATP-dependent prot
46	7	3.6	816	2	B86705	probable beta-gala
47	7	3.6	832	2	E84543	probable heme util
48	7	3.6	851	2	A83484	hypothetical prote
49	7	3.6	879	2	B84765	hypothetical prote
50	7	3.6	900	2	F71426	protein F32E10.3 (
51	7	3.6	990	2	H88733	alpha-mannosidase
52	7	3.6	1083	1	S53048	DNA-directed RNA p
53	7	3.6	1135	1	RNF32	chromosome-associa
54	7	3.6	1231	2	S70553	G-protein signalin
55	7	3.6	1387	2	JC5502	hypothetical prote
56	7	3.6	1548	2	T04456	hypothetical prote
57	7	3.6	2515	2	S47008	tenascin-like prot
58	7	3.6	4725	1	A4357	dynein heavy chain
59	6	3.1	62	2	F86783	hypothetical prote
60	6	3.1	71	2	T18866	hypothetical prote
61	6	3.1	79	2	T44223	hypothetical prote
62	6	3.1	84	2	A12925	conserved hypothet
63	6	3.1	84	2	E98356	hypothetical prote
64	6	3.1	89	2	PQ0190	pyruvate, phosphat
65	6	3.1	90	2	PQ0191	pyruvate, phosphat
66	6	3.1	96	2	A55278	homeotic protein H
67	6	3.1	99	1	H69208	hypothetical prote
68	6	3.1	99	2	A90208	embryonic abundant
69	6	3.1	102	2	S19225	hypothetical prote
70	6	3.1	102	2	T50981	hypothetical prote
71	6	3.1	104	2	D43559	homeotic protein R
72	6	3.1	107	2	A75031	lsu ribosomal prot
73	6	3.1	110	2	T00142	hypothetical prote
74	6	3.1	111	2	S41866	acidic ribosomal p
75	6	3.1	111	2	F71216	probable ribosomal
76	6	3.1	111	2	B81661	ribosomal protein
77	6	3.1	113	2	S43109	acidic ribosomal p
78	6	3.1	114	1	R5KT30	ribosomal protein
79	6	3.1	119	2	S40137	T-cell receptor V-
80	6	3.1	119	2	S24490	Ig heavy chain V r
81	6	3.1	120	2	A51030	probable membrane
82	6	3.1	120	2	T02037	acidic ribosomal p
83	6	3.1	122	2	B70026	hypothetical prote
84	6	3.1	127	2	F64039	hypothetical prote
85	6	3.1	128	2	A64335	conserved hypothet
86	6	3.1	129	2	A52132	hypothetical prote
87	6	3.1	130	2	AC1825	50S ribosomal prot
88	6	3.1	131	2	C75113	hypothetical prote
89	6	3.1	136	2	A10124	probable prelin
90	6	3.1	140	2	I47204	Ig heavy chain var
91	6	3.1	143	2	G71880	hypothetical prote
92	6	3.1	144	2	AH2443	hypothetical prote
93	6	3.1	149	2	AC0375	probable membrane
94	6	3.1	150	2	AG0564	probable membrane
95	6	3.1	151	2	G64779	probable membrane
96	6	3.1	151	2	G90697	hypothetical prote
97	6	3.1	152	2	A85548	hypothetical prote
98	6	3.1	156	2	T18755	hypothetical prote
99	6	3.1	156	2	F89418	protein B0413.7 li
100	6	3.1	162	2	E71131	hypothetical prote
101	6	3.1	163	2	B48766	ubiquitin-like pro
102	6	3.1	163	2	A48766	ubiquitin / riboso

103	6	3.1	167	2	E69768	hypothenical prote	176	6	3.1	243	2	T34680	hypothenical prote
104	6	3.1	170	2	F72115	hypothenical prote	177	6	3.1	245	2	D82305	ubiquinol-cytochro
105	6	3.1	171	2	E70395	glycine cleavage s	178	6	3.1	246	2	S58499	auxin regulated pr
106	6	3.1	172	2	S55668	hypothenical prote	179	6	3.1	249	2	D46434	iron-regulated out
107	6	3.1	173	2	T11831	NADH2 dehydrogenas	180	6	3.1	249	2	A97154	uncharacterized pt
108	6	3.1	175	2	T11151	NADH2 dehydrogenas	181	6	3.1	250	2	T20256	hypothenical prote
109	6	3.1	176	2	G70658	probable arok prot	182	6	3.1	250	2	C86338	protein F5M15.20 [
110	6	3.1	178	2	D71451	MJ0653 homolog PH0	183	6	3.1	253	2	T52380	zinc finger protei
111	6	3.1	181	2	A28782	cytochrome-c oxida	184	6	3.1	254	2	E70438	type 4 prepillin pe
112	6	3.1	181	2	A11686	hypothenical prote	185	6	3.1	257	2	G88021	hypothenical prote
113	6	3.1	182	2	S03259	methyl coenzyme M	186	6	3.1	258	2	A70468	protein W10D9.2 [i
114	6	3.1	183	2	A93262	hypothenical prote	187	6	3.1	258	2	H88130	flagellar biosynth
115	6	3.1	184	2	UC2429	activin-A protein	188	6	3.1	259	2	S76205	protein F10G7.3 [i
116	6	3.1	184	2	A83316	hypothenical prote	189	6	3.1	259	2	T49825	hypothenical prote
117	6	3.1	185	2	D96572	protein F12M15.6 [	190	6	3.1	260	2	E83092	probable cytochrom
118	6	3.1	185	2	T25098	hypothenical prote	191	6	3.1	260	2	G82166	hypothenical prote
119	6	3.1	186	2	D84673	probable calcium b	192	6	3.1	262	2	H64311	hypothetical prote
120	6	3.1	186	2	S75643	hypothenical prote	193	6	3.1	262	2	H90871	unknown protein en
121	6	3.1	188	2	S18956	fix23-4 protein -	194	6	3.1	262	2	B85747	hypothetical prote
122	6	3.1	191	2	S17505	ribonuclease - bal	195	6	3.1	262	2	T47669	hydrolase, alpha/b
123	6	3.1	191	2	AF1135	hypothenical prote	196	6	3.1	262	2	F75406	hypothetical prote
124	6	3.1	194	2	C70035	transcription regu	197	6	3.1	264	2	F7938	hypothetical prote
125	6	3.1	196	2	C84313	chemotaxis protein	198	6	3.1	264	2	T20667	hypothetical prote
126	6	3.1	197	2	F81934	probable lipoprote	199	6	3.1	265	2	T39301	probable o-methyl
127	6	3.1	198	2	C27793	methyl coenzyme M	200	6	3.1	266	2	A97980	dihydroorotate oxi
128	6	3.1	199	2	T14468	pollen coat protei	201	6	3.1	266	2	H86320	probable MYB47 tra
129	6	3.1	200	2	D64405	methyl coenzyme M	202	6	3.1	267	2	T10253	membrane protein M
130	6	3.1	200	2	F85781	hypothenical prote	203	6	3.1	269	2	B95142	vick protein (impo
131	6	3.1	200	2	B90333	hypothenical prote	204	6	3.1	269	2	T25079	hypothetical prote
132	6	3.1	202	2	S14705	chalcone isomerase	205	6	3.1	269	2	H98009	vick protein (impo
133	6	3.1	203	1	BVECKV	ruvA protein - Esc	206	6	3.1	269	2	A96011	probable cell divi
134	6	3.1	203	2	C90950	Holliday junction	207	6	3.1	271	2	T04666	hypothetical prote
135	6	3.1	203	2	G85798	Holliday junction	208	6	3.1	271	2	A86874	conserved hypotet
136	6	3.1	203	2	AC0743	Holliday junction	209	6	3.1	273	2	T07678	H+-transporting tw
137	6	3.1	204	2	S76108	hypothetical prote	210	6	3.1	277	2	AD3445	membrane protein M
138	6	3.1	204	2	A10250	Holliday junction	211	6	3.1	279	2	T10251	hypothetical prote
139	6	3.1	205	2	B95077	conserved hypotet	212	6	3.1	280	2	G96508	conserved hypotet
140	6	3.1	206	1	A55169	pre-T-cell recepto	213	6	3.1	281	2	H64058	transcription init
141	6	3.1	206	2	C29525	methyl coenzyme M	214	6	3.1	283	2	T04676	xyloglucan endo-1,
142	6	3.1	206	2	A75508	hypothetical prote	215	6	3.1	283	2	S60166	transcription init
143	6	3.1	210	2	D87507	glutathione S-tran	216	6	3.1	284	2	T03794	aquaporin NT2 - co
144	6	3.1	211	2	S37792	hypothetical prote	217	6	3.1	284	2	S04723	genome polyprotein
145	6	3.1	211	2	B83493	hypothetical prote	218	6	3.1	285	2	S60165	transcription init
146	6	3.1	213	2	J00075	neuromodulin - gol	219	6	3.1	285	2	F97311	transcription regu
147	6	3.1	213	2	B81967	cadmium resistance	220	6	3.1	286	2	T02641	probable C2H2-type
148	6	3.1	214	2	T51657	myb-related transc	221	6	3.1	286	2	G71899	hypothetical prote
149	6	3.1	217	2	T00592	GTP-binding protei	222	6	3.1	286	2	T48572	hypothetical prote
150	6	3.1	217	2	JC7997	nucleolar protein,	223	6	3.1	287	2	A60643	antigen 5401 - Elm
151	6	3.1	218	2	A75150	hypothetical prote	224	6	3.1	287	2	T09794	major intrinsic pr
152	6	3.1	218	2	T47706	hypothetical prote	225	6	3.1	288	2	F71402	xyloglucan endo-1,
153	6	3.1	219	2	T45047	hypothetical prote	226	6	3.1	289	2	F47070	CDP-abequose synth
154	6	3.1	221	2	S24784	chalcone isomerase	227	6	3.1	289	2	C71701	branched-chain ami
155	6	3.1	221	2	T47592	hypothetical prote	228	6	3.1	290	2	B97774	hypothetical prote
156	6	3.1	221	2	T12996	hypothetical prote	229	6	3.1	290	2	S23544	chitinase (EC 3.2.
157	6	3.1	222	2	T52019	ethylene responsiv	230	6	3.1	291	2	S31763	chitinase (EC 3.2.
158	6	3.1	224	2	T44351	hypothetical prote	231	6	3.1	293	2	D89193	protein T21C9.1 [i
159	6	3.1	225	2	G70340	Mg(2+) transport A	232	6	3.1	293	2	G85083	hypothetical prote
160	6	3.1	225	2	A95021	conserved hypotet	233	6	3.1	293	2	T43930	hypothetical prote
161	6	3.1	225	2	G37892	conserved hypotet	234	6	3.1	295	2	I52326	adrenocorticotropi
162	6	3.1	226	2	A26964	neuronal growth-re	235	6	3.1	296	2	JC4046	adrenocorticotropi
163	6	3.1	226	2	F71181	probable aspartate	236	6	3.1	296	2	D36788	hypothetical prote
164	6	3.1	226	2	F87449	cell division prot	237	6	3.1	297	2	S42767	hypothetical prote
165	6	3.1	228	2	G64114	CMP-NeuNAC synthet	238	6	3.1	297	2	I45849	gene ACH receptor
166	6	3.1	228	2	D86206	hypothetical prote	239	6	3.1	297	2	A98294	hypothetical prote
167	6	3.1	229	2	T29203	hypothetical prote	240	6	3.1	297	2	AH2989	permease [imported
168	6	3.1	232	2	B75157	aspartate racemase	241	6	3.1	299	2	S12022	extensin - rape
169	6	3.1	232	2	A69501	hypothetical prote	242	6	3.1	299	2	JG0178	chitinase (EC 3.2.
170	6	3.1	232	2	F75443	probable hydrolase	243	6	3.1	299	2	B75419	conserved hypotet
171	6	3.1	236	2	XJ0320	rhodanese-like pro	244	6	3.1	300	2	A45511	chitinase (EC 3.2.
172	6	3.1	239	2	S58498	IAA12 protein - Ar	245	6	3.1	302	1	S75983	hypothetical prote
173	6	3.1	239	2	G83143	hypothetical prote	246	6	3.1	303	1	T00479	probable phosphati
174	6	3.1	242	1	JWMSX3	homeotic protein H	247	6	3.1	303	2	P84998	diaminopimelate ep
175	6	3.1	243	2	F69725	tRNA methyltransfe	248	6	3.1	305	2		

249	6	3.1	306	1	H65033	hypothetical prote	322	6	3.1	352	2	C97496	hypothetical prote
250	6	3.1	306	2	C91057	hypothetical prote	323	6	3.1	354	2	C90173	3-dehydroquinat s
251	6	3.1	306	2	G85901	hypothetical prote	324	6	3.1	356	2	A46164	calnexin - human (
252	6	3.1	310	1	K10761	thymidine kinase (	325	6	3.1	356	2	B84458	hypothetical prote
253	6	3.1	311	2	T10761	chitinase (EC 3.2.	326	6	3.1	358	2	AF1457	chloromuconate cyc
254	6	3.1	312	1	S22397	pyruvate synthase	327	6	3.1	359	2	D96696	protein Fln21.8 [i
255	6	3.1	312	2	E84268	hypothetical prote	328	6	3.1	360	2	S59598	cysteine proteinas
256	6	3.1	312	2	C71806	hypothetical prote	329	6	3.1	360	2	D97501	porphobilinogen sy
257	6	3.1	312	2	G64712	toxR-activated gen	330	6	3.1	361	2	KBHH	phorbolins
258	6	3.1	312	2	E70376	exopolysphatase	331	6	3.1	361	1	S75507	aleurain (EC 3.4.2
259	6	3.1	313	2	A65140	gtmUKR operon regu	332	6	3.1	361	1	D69005	3-dehydroquinat s
260	6	3.1	315	2	T28836	hypothetical prote	333	6	3.1	361	1	D69005	hypothetical prote
261	6	3.1	315	2	AE0166	probable virulence	334	6	3.1	361	2	S68268	apurinic/apyrimidi
262	6	3.1	316	2	F83170	probable oxidoredu	335	6	3.1	363	2	H85018	hypothetical prote
263	6	3.1	316	2	D85088	nitrilase 1 like p	336	6	3.1	363	2	B48432	hypothetical prote
264	6	3.1	318	2	A81217	conserved hypothet	337	6	3.1	365	2	D97848	hypothetical prote
265	6	3.1	318	2	B81794	conserved hypothet	338	6	3.1	370	2	S77011	mercuric resistanc
266	6	3.1	320	2	S64088	probable membrane	339	6	3.1	371	2	B83781	probable 4-hydroxy
267	6	3.1	320	2	F64384	hypothetical prote	340	6	3.1	371	2	B83781	two-component sens
268	6	3.1	320	2	AF2714	conserved hypothet	341	6	3.1	373	2	AB0604	probable oxidoredu
269	6	3.1	320	2	G86010	regulator of gluc	342	6	3.1	374	2	AB4783	hypothetical prote
270	6	3.1	322	2	B96014	probable sugar upt	343	6	3.1	375	2	T33439	hypothetical prote
271	6	3.1	325	2	D87619	conserved hypothet	344	6	3.1	376	2	T39454	hypothetical prote
272	6	3.1	325	2	T18283	hypothetical prote	345	6	3.1	380	2	H75159	3-isopropylmalate
273	6	3.1	326	2	AD2353	delta-aminolevulin	346	6	3.1	380	2	B81832	probable polyamine
274	6	3.1	327	2	S75506	porphobilinogen sy	347	6	3.1	383	2	E90285	hypothetical prote
275	6	3.1	330	2	H70480	porphobilinogen sy	348	6	3.1	384	1	SUTIKA	endopeptidase K (E
276	6	3.1	330	2	E90578	30S ribosomal prot	349	6	3.1	384	2	S29130	calreticulin (clon
277	6	3.1	331	2	G91164	regulator of gluc	350	6	3.1	387	2	T17662	calreticulin prote
278	6	3.1	331	2	E84770	probable serpin [i	351	6	3.1	389	2	D90498	acyl-CoA dehydroge
279	6	3.1	334	2	H65028	probable thiosulfa	352	6	3.1	390	2	G69044	N-acetylornithine
280	6	3.1	334	2	C91052	probable thiosulfa	353	6	3.1	390	2	T21367	hypothetical prote
281	6	3.1	334	2	G85896	probable thiosulfa	354	6	3.1	395	2	S25851	calreticulin precu
282	6	3.1	334	2	A58195	Cathepsin L (EC 3.	355	6	3.1	396	2	A33880	hypothetical prote
283	6	3.1	334	2	D87416	delta-aminolevulin	356	6	3.1	397	2	D89768	syndecin 2 - human
284	6	3.1	334	2	AE3581	inositol 2-dehydro	357	6	3.1	400	1	JQ0756	hypothetical prote
285	6	3.1	335	2	C64380	porphobilinogen sy	358	6	3.1	400	2	F07055	nicotinate phospho
286	6	3.1	335	2	A72417	sugar ABC transpor	359	6	3.1	400	2	D85619	nicotinate phospho
287	6	3.1	336	2	D71016	probable thioedox	360	6	3.1	400	2	D83334	probable membrane
288	6	3.1	336	2	B69542	hypothetical prote	361	6	3.1	401	2	D83363	conserved hypothet
289	6	3.1	337	2	T24387	probable cysteine	362	6	3.1	402	2	T03567	probable integrase
290	6	3.1	337	2	AD2719	delta-aminolevulin	363	6	3.1	402	2	H81296	probable integral
291	6	3.1	337	2	A90846	hnr protein [impor	364	6	3.1	402	2	T51526	hypothetical prote
292	6	3.1	337	2	H85703	hnr protein [impor	365	6	3.1	402	2	F90035	TcAB protein [impo
293	6	3.1	337	2	A36871	37K regulator resp	366	6	3.1	403	1	G70311	histidine-tRNA lig
294	6	3.1	339	2	B69436	LSU ribosomal prot	367	6	3.1	406	2	T24273	pyruvate dehydrog
295	6	3.1	339	2	UC7112	transcription coac	368	6	3.1	407	2	T24273	hypothetical prote
296	6	3.1	340	2	E69507	signal recognition	369	6	3.1	407	2	F69865	conserved hypothet
297	6	3.1	340	2	T09416	coil protein P022,	370	6	3.1	410	2	AB0077	probable aminotran
298	6	3.1	340	2	T01949	hypothetical prote	371	6	3.1	410	2	H72502	hypothetical prote
299	6	3.1	340	2	AH1103	arginine kinase ho	372	6	3.1	411	2	S29129	calreticulin precu
300	6	3.1	340	2	AH1465	transcription regu	373	6	3.1	411	2	A70509	hypothetical prote
301	6	3.1	341	1	RPECT	probable N-acetyl	374	6	3.1	412	2	A34939	transforming growt
302	6	3.1	341	2	S91285	transcription regu	375	6	3.1	412	2	T17531	proline-rich prote
303	6	3.1	341	2	E91236	transcription regu	376	6	3.1	412	2	A83604	probable MFS trans
304	6	3.1	341	2	B86083	dihydroorotase (EC	377	6	3.1	413	2	C69160	phosphoenolpyruvat
305	6	3.1	342	2	S76410	probable acidic ri	378	6	3.1	414	2	F75087	purine-cytosine pe
306	6	3.1	342	2	G71216	hypothetical prote	379	6	3.1	414	2	T22539	hypothetical prote
307	6	3.1	344	2	T22182	galactitol-1-phosp	380	6	3.1	414	2	A39205	nuclear localizati
308	6	3.1	346	1	B84976	galactitol-1-phosp	381	6	3.1	414	2	D87448	peptidase, M20/M25
309	6	3.1	346	2	F90990	probable alcohol d	382	6	3.1	414	2	A69307	cell wall-binding
310	6	3.1	346	2	H81915	galactitol-1-phosp	383	6	3.1	415	2	C96793	unknown protein F1
311	6	3.1	346	2	H85835	hypothetical prote	384	6	3.1	419	2	A47033	chloramphenicol re
312	6	3.1	346	2	H72237	hypothetical prote	385	6	3.1	419	2	JQ1201	CmlA protein - Pse
313	6	3.1	346	2	A83725	chemotaxis protein	386	6	3.1	419	2	E69888	metabolite transpo
314	6	3.1	347	2	G83026	hypothetical prote	387	6	3.1	420	2	S45630	DNA primase chain
315	6	3.1	347	2	T24921	probable alcohol d	388	6	3.1	420	2	T45592	hypothetical prote
316	6	3.1	348	1	H81186	probable arsenical	389	6	3.1	420	2	C84201	multidrug resistan
317	6	3.1	349	1	E64442	conserved hypothet	390	6	3.1	420	2	T41236	conserved hypothet
318	6	3.1	349	2	E89795	hypothetical 39K p	391	6	3.1	421	2	A24830	phosphoglycerate k
319	6	3.1	349	2	JH0235	thymidine kinase (	392	6	3.1	421	2	D95975	hypothetical outer
320	6	3.1	350	1	K1BEFC	adenosine deaminas	393	6	3.1	422	2	A71058	probable cytosine
321	6	3.1	352	2	G86660		394	6	3.1	422	2	C70046	macrolide-efflux p

395	6	3.1	427	2	G59067	N-ethylmelamine ch	468	1	502	1	S45039	cytochrome P450 -
396	6	3.1	427	2	A11131	permeases homolog	469	6	502	2	A84582	hexokinase (ATHKX2
397	6	3.1	427	2	A11191	permeases homolog	470	6	504	2	S33190	phase-1 flagellin
398	6	3.1	427	2	S38032	hypothetical prote	471	6	505	2	B64560	poly E-rich protei
399	6	3.1	428	2	T47400	hypothetical prote	472	6	505	2	S75961	NADH2 dehydrogenas
400	6	3.1	429	1	S18489	phosphoribosylamin	473	6	507	2	S33192	phase-1 flagellin
401	6	3.1	429	2	AC0391	phosphoribosylglyc	474	6	507	2	S33185	phase-1 flagellin
402	6	3.1	430	2	D22402	UDP-N-acetylmuramo	475	6	507	2	T48645	glycine betaine tr
403	6	3.1	430	2	AD0138	tolB colicin impor	476	6	507	2	AD1336	glycine betaine tr
404	6	3.1	431	2	G75108	pyridoxal-phosphat	477	6	507	2	G87466	tryptophan halogen
405	6	3.1	431	2	G75108	probable aspartoki	478	6	508	2	A53465	phase 1 flagellin
406	6	3.1	431	2	G84276	hypothetical prote	479	6	508	2	E72299	glutamate synthase
407	6	3.1	431	2	F84375	N-ethylmelamine ch	480	6	509	2	T06300	hypothetical prote
408	6	3.1	431	2	UC7730	1-aminocyclopropan	481	6	509	2	G96552	unknown protein, 6
409	6	3.1	433	2	S37790	probable serine/th	482	6	510	2	G73606	tryptophan halogen
410	6	3.1	435	2	A82554	conserved hypoteth	483	6	511	2	T36306	hypothetical prote
411	6	3.1	436	2	T30911	xylanase (EC 3.2.1	484	6	512	2	G87369	probable anthranil
412	6	3.1	437	1	B69448	ribulose-bisphosph	485	6	513	1	A47436	hypothetical prote
413	6	3.1	438	2	E87616	hypothetical prote	486	6	513	2	S75997	1,25-dihydroxyvita
414	6	3.1	438	2	S64917	hypothetical prote	487	6	513	2	A95154	asparagine-tRNA li
415	6	3.1	440	2	IS5442	peroxisome prolif	488	6	519	2	AH0064	sodium/solute symp
416	6	3.1	440	2	UC4530	nitrilase/Fhlt pro	489	6	525	2	G84406	thiamin transport
417	6	3.1	440	2	T43198	hypothetical prote	490	6	525	2	B82293	halolysin [impor
418	6	3.1	440	2	B71153	steroid hormone re	491	6	526	2	C84223	MvIN protein VC068
419	6	3.1	441	2	A45360	mitosis-specific c	492	6	526	2	A75581	methylmalonyl-CoA
420	6	3.1	443	2	T14916	conserved hypoteth	493	6	528	2	T34417	flavin monooxime o
421	6	3.1	444	2	B83249	glutamate-ammonia	494	6	528	2	T42234	delayed rectifier
422	6	3.1	445	2	A48947	beta-tubulin 1 - a	495	6	529	1	VGNZSP	cell fusion glycop
423	6	3.1	445	2	JQ0422	protein T01B7.5 (l	496	6	530	2	T16263	cof head-related
424	6	3.1	445	2	H88244	mitosis-specific c	497	6	531	2	T16263	hypothetical prote
425	6	3.1	446	2	T03021	hypothetical prote	498	6	531	2	B70400	phage related prot
426	6	3.1	447	2	T02547	hypothetical prote	499	6	534	2	F84398	phosphate ABC tran
427	6	3.1	448	2	T36597	hypothetical prote	500	6	535	2	S61185	hypothetical prote
428	6	3.1	449	2	F84241	hypothetical prote	501	6	535	2	F81094	pyruvate dehydrog
429	6	3.1	452	2	T36042	probable plasmid r	502	6	535	2	F81847	alkaline serine pr
430	6	3.1	452	2	T05699	hypothetical prote	503	6	536	1	C64728	dihydrolipoamide S
431	6	3.1	453	2	D86759	hypothetical prote	504	6	536	2	G85488	probable membrane
432	6	3.1	453	2	A97431	alpha-glucosidase-b	505	6	536	2	G90637	probable transport
433	6	3.1	453	2	AB2649	hypothetical prote	506	6	536	2	GH0515	probable transport
434	6	3.1	454	2	T02593	hypothetical prote	507	6	542	2	T06728	pectate lyase (EC
435	6	3.1	455	2	G75473	probable carotenoi	508	6	546	2	S67292	probable membrane
436	6	3.1	458	2	H82504	conserved hypoteth	509	6	552	2	S46809	hypothetical prote
437	6	3.1	459	2	C81195	spexmidine/putresc	510	6	552	2	E72283	alpha-galactosidas
438	6	3.1	460	2	A39338	phosphotransferase	511	6	555	2	C72512	probable thermosom
439	6	3.1	460	2	G90890	hypothetical prote	512	6	556	2	A6024	neurofilament-l su
440	6	3.1	460	2	B85727	hypothetical prote	513	6	559	2	AG2471	two-component sens
441	6	3.1	460	2	E64902	hypothetical prote	514	6	560	1	F69059	arginine-tRNA liga
442	6	3.1	461	2	G59093	hypothetical prote	515	6	560	2	TS2438	PRM1 homolog [impo
443	6	3.1	461	2	A60746	chromogranin A pre	516	6	562	2	S78099	furostanol glycosi
444	6	3.1	462	1	T26195	hypothetical prote	517	6	562	2	E64412	hypothetical prote
445	6	3.1	467	2	T26195	probable selenium-	518	6	565	2	T47775	DNA ligase (EC 6.5
446	6	3.1	469	2	T02325	metalloelastase HM	519	6	565	2	T47775	methyl-accepting c
447	6	3.1	470	2	A49499	PRM1 homolog [impo	520	6	570	2	F70332	proline-tRNA synth
448	6	3.1	470	2	AE1930	ammonium transport	521	6	570	2	S07330	keratin, epidermal
449	6	3.1	471	2	AB2266	trigger factor [im	522	6	572	2	S42866	serine/threonine p
450	6	3.1	471	2	AB2266	probable MFS trans	523	6	572	2	B84958	proline-tRNA ligas
451	6	3.1	471	2	S05392	hypothetical prote	524	6	574	2	S58992	NADH2 dehydrogenas
452	6	3.1	476	2	AF0765	undecaprenyl-phosp	525	6	575	2	T34280	hypothetical prote
453	6	3.1	482	1	ZPBX	mitochondrial proc	526	6	577	2	T22460	hypothetical prote
454	6	3.1	482	1	AD2515	hypothetical prote	527	6	579	2	T13004	cell division cycl
455	6	3.1	483	2	T20895	hypothetical prote	528	6	580	2	C96597	Rubisco subunit bi
456	6	3.1	483	2	S43737	protein kinase SLR	529	6	580	2	T43210	fibulin-1D precurs
457	6	3.1	488	2	G81363	probable amino-aci	530	6	589	2	T43210	keratin 5, type II
458	6	3.1	491	2	G95105	lysine decarboxyla	531	6	591	2	A75474	serine proteinase,
459	6	3.1	491	2	H97973	lysine decarboxyla	532	6	591	2	T53260	probable thiol-dis
460	6	3.1	491	2	C96585	hypothetical prote	533	6	592	2	E83039	calnexin - human
461	6	3.1	492	1	S68968	trypanothione-disu	534	6	592	2	A37273	calnexin precursor
462	6	3.1	492	1	S28003	trypanothione-disu	535	6	593	1	A37273	calnexin precursor
463	6	3.1	492	1	T06875	preproteins translo	536	6	600	2	E87665	arginyl-tRNA synth
464	6	3.1	494	1	WJFEBC	homeotic protein b	537	6	601	2	E87028	pyruvate, phosphat
465	6	3.1	494	2	E83254	guananyl-tRNA synt	538	6	603	2	B83022	transport protein
466	6	3.1	498	2	PC6300	synaptotagmin X -	539	6	607	2	F82966	probable transcarb
467	6	3.1	500	2	S41859	xylan 1,4-beta-xy	540	6	607	2	F82966	

541	6	3.1	608	2	T19437	hypothetical prote	614	3.1	755	2	T47806	hypothetical prote
542	6	3.1	611	2	D81347	arginine decarboxy	615	3.1	758	2	T02925	protoporphyrin IX
543	6	3.1	611	2	T20501	hypothetical prote	616	3.1	758	2	A98290	expolysaccharide
544	6	3.1	612	2	F70325	conserved hypotet	617	3.1	758	2	AB2994	hypothetical prote
545	6	3.1	612	2	T11628	MVP1 protein - fls	618	3.1	760	2	T24521	hypothetical prote
546	6	3.1	613	2	S57687	probable membrane	619	3.1	763	2	T08929	hypothetical prote
547	6	3.1	614	1	QRECBT	vitamin B12 recept	620	3.1	768	2	G82506	GTP pyrophosphokin
548	6	3.1	614	2	A98241	hypothetical prote	621	3.1	769	2	D81828	structural polypro
549	6	3.1	614	2	F86088	hypothetical prote	622	3.1	773	2	A47666	xylosidase - Therm
550	6	3.1	614	2	AB0935	vitamin B12 recept	623	3.1	778	2	D72421	sporulation protei
551	6	3.1	614	2	S27962	modulator recognit	624	3.1	778	2	S43132	probable polyprote
552	6	3.1	618	1	S38004	probable transpor	625	3.1	778	2	D85055	formate dehydrogen
553	6	3.1	618	2	A83074	hypothetical prote	626	3.1	782	2	B83966	hypothetical prote
554	6	3.1	619	2	T34451	hypothetical prote	627	3.1	786	2	T26811	hypothetical prote
555	6	3.1	621	2	S73155	hypothetical prote	628	3.1	786	2	F70735	hypothetical prote
556	6	3.1	622	2	T37204	hypothetical prote	629	3.1	792	2	S72831	cadherin 12 - huma
557	6	3.1	622	2	C84506	probable Achia re	630	3.1	794	2	I59372	hypothetical prote
558	6	3.1	622	2	AC1236	acyltransferase (c	631	3.1	802	2	T05596	probable potassium
559	6	3.1	627	2	B44409	gamma-aminobutyric	632	3.1	805	2	E70474	translation initia
560	6	3.1	627	2	JH0695	probable biotin-pr	633	3.1	805	2	A10176	probable oxidoredu
561	6	3.1	631	2	T40189	hypothetical prote	634	3.1	805	2	T40275	probable glutaminy
562	6	3.1	633	2	T52506	hypothetical prote	635	3.1	811	2	F71880	unknown protein [i
563	6	3.1	633	2	G96503	protein F9C16.15 [	636	3.1	815	2	F71880	probable ATP-depen
564	6	3.1	633	2	AH1598	acyltransferase (c	637	3.1	816	2	D96544	heat shock protein
565	6	3.1	634	2	C69975	acyltransferase ho	638	3.1	817	2	F83073	adipocyte transcri
566	6	3.1	638	2	S51266	trsg protein - Yer	639	3.1	823	2	T09882	probable transcrip
567	6	3.1	638	2	T73709	flr-1 protein - Ca	640	3.1	845	2	T40824	neurofilament trip
568	6	3.1	638	2	T44763	conserved hypotet	641	3.1	857	2	S15762	chitinase (EC 3.2.
569	6	3.1	639	2	D70720	hypothetical prote	642	3.1	858	2	JC4566	lipoxigenase (EC 1
570	6	3.1	641	2	PH1919	FL-160-4 protein -	643	3.1	860	2	S07075	hypothetical prote
571	6	3.1	644	2	S55395	neurofilament prot	644	3.1	864	1	G71891	ATP-dependent RNA
572	6	3.1	646	2	T31599	hypothetical prote	645	3.1	868	2	F71092	ubiquitin-specific
573	6	3.1	646	2	JC5583	85K SH3 domain-con	646	3.1	873	2	T50182	allanyl-tRNA synth
574	6	3.1	652	2	I48083	amphotropic murine	647	3.1	881	2	A97107	spindle pole body-
575	6	3.1	657	2	C89815	methionyl-tRNA syn	648	3.1	882	2	T43250	DNA-directed RNA p
576	6	3.1	659	1	B44212	structural protein	649	3.1	885	1	S26723	probable adenylate
577	6	3.1	659	2	T33557	hypothetical prote	650	3.1	886	2	T40734	hypothetical prote
578	6	3.1	660	1	VHWHT2	structural protein k	651	3.1	891	2	B97759	cell wall-associat
579	6	3.1	660	2	T45569	receptor protein k	652	3.1	894	2	F69730	hypothetical prote
580	6	3.1	664	2	D96633	hypothetical prote	653	3.1	897	2	S50350	aconitate hydratase
581	6	3.1	670	1	H70421	hypothetical prote	654	3.1	901	2	F89910	DNA polymerase I (
582	6	3.1	670	2	T06742	hypothetical prote	655	3.1	908	2	C70158	hypothetical prote
583	6	3.1	674	2	G72204	hypothetical prote	656	3.1	909	2	G69599	aconitate hydratase
584	6	3.1	676	1	S69783	outer membrane pro	657	3.1	911	2	T18451	hypothetical prote
585	6	3.1	680	2	T19939	hypothetical prote	658	3.1	912	2	A54423	brevican precursor
586	6	3.1	683	2	D90327	n-methylhydantoina	659	3.1	913	2	T52485	neurofilament prot
587	6	3.1	689	2	T42760	fibulin, splice fo	660	3.1	914	2	T17233	serine/threonine p
588	6	3.1	690	2	A83441	potassium-transpor	661	3.1	915	2	T51600	hypothetical prote
589	6	3.1	693	2	T13175	NADH2 dehydrogenas	662	3.1	942	2	A96748	pyruvate, phosphat
590	6	3.1	699	2	S67773	hypothetical prote	663	3.1	946	2	K12MPO	metal-transporting
591	6	3.1	708	2	S70834	transcription init	664	3.1	947	1	T06003	Mic1 protein - yea
592	6	3.1	709	2	D92825	conserved hypotet	665	3.1	949	2	S64405	hypothetical prote
593	6	3.1	711	2	T27358	hypothetical prote	666	3.1	950	2	T24866	hypothetical prote
594	6	3.1	712	2	T42990	fibulin 1, splice	667	3.1	971	2	T14076	probable villin li
595	6	3.1	714	2	A83314	probable chemotaxi	668	3.1	974	2	T47518	serine/threonine p
596	6	3.1	715	2	D85087	hypothetical prote	669	3.1	996	2	F81731	glycyl-tRNA synthe
597	6	3.1	723	2	T47613	ABC transporter-li	670	3.1	1003	2	B71469	glycine-tRNA ligase
598	6	3.1	724	2	S42868	serine/threonine p	671	3.1	1004	2	A55142	myosin-light-chain
599	6	3.1	726	2	B86202	hypothetical prote	672	3.1	1017	2	T37201	hypothetical prote
600	6	3.1	728	1	HHCH90	heat shock protein	673	3.1	1021	2	B85023	probable membrane
601	6	3.1	731	2	T08855	nephrocystin - hum	674	3.1	1025	2	S54044	probable GTPase ac
602	6	3.1	733	2	S31288	MAK10 protein - ye	675	3.1	1031	2	T38411	hypothetical prote
603	6	3.1	735	2	G02937	fertilin beta - cr	676	3.1	1032	2	T42701	preproteins translo
604	6	3.1	735	2	T49622	hypothetical prote	677	3.1	1036	2	A57386	hypothetical prote
605	6	3.1	735	2	S74209	multifunctional be	678	3.1	1038	1	XPEEA9	large structural p
606	6	3.1	736	2	G01522	acidic 82 kDa prot	679	3.1	1048	1	XPEEA9	serine/threonine-s
607	6	3.1	736	2	S51936	estradiol 17beta-d	680	3.1	1051	1	JW0051	retrovirus-related
608	6	3.1	737	2	F81049	GTP pyrophosphokin	681	3.1	1059	2	B4872	arachidonate 8-lip
609	6	3.1	740	2	T09480	hypothetical prote	682	3.1	1066	2	T30903	SKI2 protein homol
610	6	3.1	740	2	T26140	hypothetical prote	683	3.1	1073	1	S56822	cobN protein homol
611	6	3.1	748	2	A64319	carbon-monoxide de	684	3.1	1085	2	T03531	
612	6	3.1	752	2	S64750	probable ATP-depen	685	3.1				
613	6	3.1	754	2	A84473	probable serine pr	686	3.1				

687	6	3.1	1087	2	T30330	gelsolin-related p	760	5	2.6	24	2	S02073	photosystem II 10K
688	6	3.1	1087	2	T31100	probable potassium	761	5	2.6	27	4	JE0015	probable 2.8K prot
689	6	3.1	1110	2	I51116	NF-180 - sea lamp	762	5	2.6	33	2	T06843	probable plastocqui
690	6	3.1	1112	2	T40382	dna repair protein	763	5	2.6	36	2	S38517	mablin II chain
691	6	3.1	1113	2	T00736	hypothetical prote	764	5	2.6	36	2	A60343	transforming prote
692	6	3.1	1113	2	S30301	excision repair pr	765	5	2.6	43	1	I39482	MSL leader peptide
693	6	3.1	1113	2	T49517	p63 related protei	766	5	2.6	43	1	C25028	hypothetical eryth
694	6	3.1	1132	2	T03844	telomerase catalyt	767	5	2.6	43	1	S49317	MSL leader peptide
695	6	3.1	1132	2	S51855	hypothetical prote	768	5	2.6	43	1	I40879	hypothetical prote
696	6	3.1	1183	2	F84669	probable chromosom	769	5	2.6	45	2	T52276	RNA-binding protei
697	6	3.1	1186	2	TNBBEG	DNA-binding protei	770	5	2.6	45	2	S28838	hypothetical prote
698	6	3.1	1192	2	T13424	hypothetical prote	771	5	2.6	46	2	AF1063	hypothetical prote
699	6	3.1	1197	2	A48350	DNA-binding protei	772	5	2.6	47	2	A37174	dihydrofolate redu
700	6	3.1	1201	2	H69898	hypothetical prote	773	5	2.6	50	2	T09004	hypothetical prote
701	6	3.1	1209	2	AH2052	hypothetical prote	774	5	2.6	51	2	T35701	streptococci A-Ff
702	6	3.1	1246	2	T00406	hypothetical prote	775	5	2.6	51	2	T09004	hypothetical prote
703	6	3.1	1257	2	I58383	retinoblastoma bin	776	5	2.6	54	2	C71570	probable serine pr
704	6	3.1	1257	2	T09493	period protein hom	777	5	2.6	54	2	T36552	hypothetical prote
705	6	3.1	1264	2	H96498	hypothetical prote	778	5	2.6	55	2	D32052	hypothetical prote
706	6	3.1	1270	2	T22615	hypothetical prote	779	5	2.6	55	2	A82912	fixs protein - Rhi
707	6	3.1	1271	2	T08607	hypothetical prote	780	5	2.6	55	2	S51417	ribosomal protein
708	6	3.1	1282	2	JE0120	glycoprotein A - m	781	5	2.6	55	2	B95344	fixs1 nitrogen fix
709	6	3.1	1290	2	S73653	DNA-directed RNA p	782	5	2.6	55	2	E81417	small hydrophobic
710	6	3.1	1298	2	I54367	X-linked nuclear p	783	5	2.6	55	2	B97548	hypothetical prote
711	6	3.1	1333	2	E84601	probable retroelem	784	5	2.6	56	2	I54423	MHC class II DOB2
712	6	3.1	1337	2	T13948	atypical protein k	785	5	2.6	56	2	T34739	tropoin 1 3, fast
713	6	3.1	1351	2	C71607	hypothetical prote	786	5	2.6	56	2	JW0095	hydrophobic protei
714	6	3.1	1353	2	T00347	hypothetical prote	787	5	2.6	56	2	AD2498	P5 protein - human
715	6	3.1	1357	2	T29465	hypothetical prote	788	5	2.6	56	2	T43241	hypothetical prote
716	6	3.1	1367	2	T38820	probable calcium-t	789	5	2.6	58	2	E95595	probable ribosomal
717	6	3.1	1386	2	T00257	hypothetical prote	790	5	2.6	58	2	S58143	unknown protein, 2
718	6	3.1	1388	2	A57655	tim (timeless) pro	791	5	2.6	58	2	A45824	gene 14 protein -
719	6	3.1	1426	2	A99580	hypothetical prote	792	5	2.6	58	2	AF1401	ribosomal protein
720	6	3.1	1436	2	UC5290	protein-tyrosine-p	793	5	2.6	59	2	AF1401	ribosomal protein
721	6	3.1	1442	2	S72441	protein-tyrosine-p	794	5	2.6	59	2	D82505	hypothetical prote
722	6	3.1	1458	2	T51995	hypothetical prote	795	5	2.6	59	2	B82207	hypothetical prote
723	6	3.1	1458	2	T39266	probable cell cycl	796	5	2.6	60	2	G97044	hypothetical prote
724	6	3.1	1553	2	T03301	rab3 effector prot	797	5	2.6	61	2	T40671	60S ribosomal prot
725	6	3.1	1558	2	B71603	RBSA-H3 antigen PF	798	5	2.6	61	2	A64789	ylcE protein - Esc
726	6	3.1	1583	2	S59644	sister chromatid c	799	5	2.6	62	2	T13997	aquaporin - common
727	6	3.1	1584	2	T00026	brain-specific ang	800	5	2.6	62	2	H64443	hypothetical prote
728	6	3.1	1641	2	T38614	helicase II - huma	801	5	2.6	62	2	S40758	hypothetical prote
729	6	3.1	1743	2	T26859	complement C4A pre	802	5	2.6	65	2	A59222	neurotoxin X - sco
730	6	3.1	1744	2	C4HU	hypothetical prote	803	5	2.6	66	2	T35138	hypothetical prote
731	6	3.1	2076	2	T28915	hypothetical prote	804	5	2.6	66	2	S48660	M-like protein enn
732	6	3.1	2172	2	T20145	hypothetical prote	805	5	2.6	67	2	S61817	tropoin 1 1, fast
733	6	3.1	2210	2	RXPPTV	genome polyprotein	806	5	2.6	67	2	G84255	GPI-anchored epidi
734	6	3.1	2254	2	D86215	protein T6D22.14 [	807	5	2.6	67	2	I69230	probable membrane
735	6	3.1	2257	2	A57710	acetyl-CoA carboxy	808	5	2.6	67	2	B81328	hypothetical prote
736	6	3.1	2493	2	S26372	nonstructural poly	809	5	2.6	67	2	AH1921	hypothetical prote
737	6	3.1	2493	2	S72349	nonstructural poly	810	5	2.6	67	2	JC6521	metallothionein II
738	6	3.1	2499	2	A30788	mannose 6-phosphat	811	5	2.6	68	2	B65945	hypothetical prote
739	6	3.1	2649	2	A40937	bullous pemphigoid	812	5	2.6	69	2	B97230	hypothetical prote
740	6	3.1	2722	2	T20532	hypothetical prote	813	5	2.6	69	2	B64497	hypothetical prote
741	6	3.1	2738	2	E88320	protein F07A11.6 [	814	5	2.6	70	2	G82833	hypothetical prote
742	6	3.1	3282	2	E82750	hemagglutinin-like	815	5	2.6	70	2	S15869	seed storage prote
743	6	3.1	3386	2	GNWVDF	genome polyprotein	816	5	2.6	70	2	A59346	ribosomal protein
744	6	3.1	3442	2	E82589	hemagglutinin-like	817	5	2.6	71	1	S15869	hypothetical prote
745	6	3.1	3455	2	E82519	hemagglutinin-like	818	5	2.6	71	1	G84978	hypothetical prote
746	6	3.1	3498	2	T22330	hypothetical prote	819	5	2.6	71	2	G72226	hypothetical prote
747	6	3.1	4967	2	S72269	ryanodine receptor	820	5	2.6	71	2	D82541	hypothetical prote
748	6	3.1	4969	2	A37113	ryanodine receptor	821	5	2.6	71	2	S28843	ribosomal protein
749	6	3.1	5032	2	A35041	ryanodine receptor	822	5	2.6	71	2	S78193	mablin II chain
750	6	3.1	5035	2	I46646	ryanodine receptor	823	5	2.6	72	2	S05485	hypothetical prote
751	6	3.1	5037	2	B35041	hypothetical prote	824	5	2.6	72	2	E43259	hypothetical prote
752	6	3.1	7829	2	T15789	hypothetical prote	825	5	2.6	72	2	H71149	hypothetical prote
753	6	3.1	9376	2	T14593	syringomycin synth	826	5	2.6	73	2	T31216	hypothetical prote
754	5	2.6	10	2	E60527	sperm-activating p	827	5	2.6	73	2	F85554	insulin-like growt
755	5	2.6	10	2	C60588	sperm-activating p	828	5	2.6	73	2	C23734	hypothetical prote
756	5	2.6	19	2	JP0057	ribosomal protein	829	5	2.6	74	2	S10868	hypothetical prote
757	5	2.6	20	2	S71593	serine proteinase	830	5	2.6	74	2	A43921	dihydropyridine re
758	5	2.6	20	2	A54077	cytochrome b558 -	831	5	2.6	74	2	A43921	M-like protein pre
759	5	2.6	20	2	JP0056	ribosomal protein	832	5	2.6	75	2	S62073	



833	5	2.6	75	2	E69508	conserved hypothet	906	5	2.6	88	2	A84166	hypothetical prote
834	5	2.6	75	2	C95197	hypothetical prote	907	5	2.6	88	2	A83241	hypothetical prote
835	5	2.6	75	2	A86883	hypothetical prote	908	5	2.6	88	2	T30626	hypothetical prote
836	5	2.6	75	2	T30286	hypothetical prote	909	5	2.6	88	2	D86013	hypothetical prote
837	5	2.6	75	2	H70966	hypothetical prote	910	5	2.6	89	2	S38701	MHC class II histo
838	5	2.6	75	2	H98063	hypothetical prote	911	5	2.6	89	2	S38702	MHC class II histo
839	5	2.6	75	2	AG2371	hypothetical prote	912	5	2.6	89	2	S38704	MHC class II histo
840	5	2.6	76	1	W7WLB4	E7 protein - bovin	913	5	2.6	89	2	PL0129	class II histocomp
841	5	2.6	76	2	I68907	MHC protein - cott	914	5	2.6	89	2	G53226	retrovirus-related
842	5	2.6	76	2	I68920	MHC protein - cott	915	5	2.6	89	2	A90820	hypothetical prote
843	5	2.6	76	2	I68915	M protein precurs	916	5	2.6	89	2	T14959	hypothetical prote
844	5	2.6	76	2	S60789	hypothetical prote	917	5	2.6	90	1	R3RZ15	ribosomal protein
845	5	2.6	77	2	H81214	hypothetical prote	918	5	2.6	90	1	R3RZ15	ribosomal protein
846	5	2.6	77	2	E82407	hypothetical prote	919	5	2.6	90	1	A34435	ribosomal protein
847	5	2.6	77	2	T35645	GTP-binding protei	920	5	2.6	90	2	S68801	acetylcholinestera
848	5	2.6	78	2	S72519	GTP-binding protei	921	5	2.6	90	2	A24629	Ig gamma-3 chain C
849	5	2.6	78	2	S78474	GTP-binding protei	922	5	2.6	90	2	S62081	M-like protein pre
850	5	2.6	78	2	S72518	hypothetical prote	923	5	2.6	90	2	B75304	hypothetical prote
851	5	2.6	78	2	D64590	hypothetical prote	924	5	2.6	91	2	SL7627	Ig kappa chain V r
852	5	2.6	79	2	B97027	feolA-like protein,	925	5	2.6	91	2	SL7628	Ig kappa chain V r
853	5	2.6	79	2	T07352	translation initia	926	5	2.6	91	2	SL7629	Ig kappa chain V r
854	5	2.6	79	2	A90171	SSU ribosomal prot	927	5	2.6	91	2	SL7637	Ig kappa chain V r
855	5	2.6	79	2	TL7523	hypothetical prote	928	5	2.6	91	2	SL7638	Ig kappa chain V r
856	5	2.6	79	2	B64614	hypothetical prote	929	5	2.6	91	2	SL7639	Ig kappa chain V r
857	5	2.6	79	2	C71901	hypothetical prote	930	5	2.6	92	2	AB2021	hypothetical prote
858	5	2.6	79	2	E69854	hypothetical prote	931	5	2.6	92	2	S55663	hypothetical prote
859	5	2.6	79	2	AE2014	hypothetical prote	932	5	2.6	93	2	A97421	PH adaptation pota
860	5	2.6	80	2	S60835	M protein precurs	933	5	2.6	93	2	AH2638	transcription regu
861	5	2.6	80	2	I39417	epidermal growth f	934	5	2.6	93	2	A33472	phage related prot
862	5	2.6	80	2	I49469	epidermal growth f	935	5	2.6	93	2	AB1729	exo-alpha-sialidas
863	5	2.6	80	2	AC2394	hypothetical prote	936	5	2.6	94	2	A00888	histone-like prote
864	5	2.6	80	2	AI2504	hypothetical prote	937	5	2.6	94	2	D82712	DNA binding protei
865	5	2.6	81	2	S22455	hypothetical prote	938	5	2.6	94	2	AH2297	virulence associat
866	5	2.6	81	2	A82251	molybdenum cofacto	939	5	2.6	94	2	T09450	virulence associat
867	5	2.6	81	2	E71523	hypothetical prote	940	5	2.6	94	2	C64559	M protein precurs
868	5	2.6	82	1	QFBO	micro glutamic aci	941	5	2.6	94	2	S60794	papx protein - Esc
869	5	2.6	82	2	S61822	M-like protein enn	942	5	2.6	94	2	T02230	hypothetical prote
870	5	2.6	82	2	S71166	RNA-directed DNA p	943	5	2.6	94	2	T28763	transcription regu
871	5	2.6	82	2	A99836	hypothetical prote	944	5	2.6	95	2	D84117	Ig kappa chain V r
872	5	2.6	82	2	T41857	hypothetical prote	945	5	2.6	95	2	D33730	acyl carrier prote
873	5	2.6	82	2	C85694	unknown protein en	946	5	2.6	95	2	A47030	probable sigma-54
874	5	2.6	83	2	F71517	probable L27 ribos	947	5	2.6	95	2	G82065	hypothetical prote
875	5	2.6	83	2	E81673	ribosomal protein	948	5	2.6	95	2	A82453	hypothetical prote
876	5	2.6	83	2	A45466	glycine/tyrosine-r	949	5	2.6	95	2	T46086	hypothetical prote
877	5	2.6	83	2	H84098	hypothetical prote	950	5	2.6	95	2	H97031	hypothetical prote
878	5	2.6	84	1	TPPG	insulin precursor	951	5	2.6	96	1	CCQFF2	cytochrome c2, iso
879	5	2.6	84	2	S06077	H+-transporting tw	952	5	2.6	96	1	S49144	amoebapore B precu
880	5	2.6	84	2	T24385	hypothetical prote	953	5	2.6	96	1	MFIV2K	matrix protein M2
881	5	2.6	84	2	A89984	hypothetical prote	954	5	2.6	96	1	MFIV2F	matrix protein M2
882	5	2.6	85	2	H82952	atp synthase C cha	955	5	2.6	96	1	ZEBPG4	gene B protein - p
883	5	2.6	85	2	H84728	hypothetical prote	956	5	2.6	96	2	S11219	nonhistone chromos
884	5	2.6	85	2	H69191	hypothetical prote	957	5	2.6	96	2	S60842	M protein precurs
885	5	2.6	85	2	T16045	hypothetical prote	958	5	2.6	96	2	S61804	M-like protein enn
886	5	2.6	85	2	S00071	keratin high-tyros	959	5	2.6	96	2	R82311	conserved hypothet
887	5	2.6	86	1	ZCBPF4	gene C protein - p	960	5	2.6	96	2	A87110	conserved hypothet
888	5	2.6	86	2	S07119	ribulose-bisphosph	961	5	2.6	96	2	F64319	hypothetical prote
889	5	2.6	86	2	S53701	ribosomal protein	962	5	2.6	96	2	AE2692	hypothetical prote
890	5	2.6	86	2	J50453	gene C protein - p	963	5	2.6	97	1	CCQFM2	cytochrome c2, iso
891	5	2.6	86	2	C90666	probable DNA bindi	964	5	2.6	97	1	MMIV2	matrix protein M2
892	5	2.6	86	2	G85516	probable ATP bindi	965	5	2.6	97	1	MFIV62	matrix protein M2
893	5	2.6	86	2	G30675	probable ATP bindi	966	5	2.6	97	1	MFIV2M	matrix protein M2
894	5	2.6	86	2	D64016	hypothetical prote	967	5	2.6	97	1	PN0084	matrix protein M2
895	5	2.6	86	2	C97083	uncharacterized pr	968	5	2.6	97	1	C45539	matrix protein M2
896	5	2.6	86	2	B85526	probable ATP bindi	969	5	2.6	97	1	S18023	matrix protein M2
897	5	2.6	87	2	S26282	retrovirus-related	970	5	2.6	97	2	S26341	ribulose-bisphosph
898	5	2.6	87	2	D95032	conserved hypothet	971	5	2.6	97	2	PH1084	Ig light chain V r
899	5	2.6	87	2	D37903	hypothetical prote	972	5	2.6	97	2	S36066	Ig light chain V r
900	5	2.6	88	2	S03442	class II histocomp	973	5	2.6	97	2	S61811	M-like protein enn
901	5	2.6	88	2	S60837	M protein precurs	974	5	2.6	97	2	S04057	matrix protein M2
902	5	2.6	88	2	H47759	retrovirus-related	975	5	2.6	97	2	S04061	matrix protein M2
903	5	2.6	88	2	G42465	hypothetical prote	976	5	2.6	97	2	S14617	matrix protein M2
904	5	2.6	88	2	UJ0029	hypothetical 9.7K	977	5	2.6	97	2	S04051	matrix protein M2
905	5	2.6	88	2	D91167	hypothetical prote	978	5	2.6	97	2		

## ALIGNMENTS

[illegible]

Nature 408, 818-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A:Reference number: AB6141; MUID:21016719; PMID:11130712  
A:Accession: C96545  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-768 <STO>  
A:Cross-references: GB:AE005173; NID:q11094697; PIDN:AG29633.1; GSPDB:GN00141

```
C90342
hypothetical protein SS08938 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: C90342
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90342
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: GB:AE006641; NID:gl3815050; PIDN:AAK41994.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS08938

Query Match 3.6%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 MPRPGYK 81
DB 1 MPRPGYK 7

RESULT 8
RS9YIB
acidic ribosomal protein P2.e.A, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: acidic ribosomal protein A2; acidic ribosomal protein P2.beta; protein
C:Species: Saccharomyces cerevisiae
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jul-2000
C:Accession: B28104; S00679; B35109; S66724; A49495
R:Remacha, M.; Saenz-Robles, M.T.; Vilella, M.D.; Ballesta, J.P.G.
J. Biol. Chem. 263, 9094-9101, 1988
A:Title: Independent genes coding for three acidic proteins of the large ribosomal subunit
A:Reference number: A92726; MUID:88243786; PMID:2837476
A:Accession: B28104
A:Molecule type: DNA
A:Residues: 1-106 <REM>
A:Cross-references: EMBL:J03760; NID:gl72395; PIDN:AAA4971.1; PID:gl72396
R:Mitsui, K.; Tsurugi, K.
Nucleic Acids Res. 16, 3575, 1988
A:Title: cDNA and deduced amino acid sequence of acidic ribosomal protein A2 from Sacchar
A:Reference number: S00679; MUID:88233944; PMID:3287329
A:Accession: S00679
A:Molecule type: mRNA
A:Residues: 1-106 <MIT>
A:Cross-references: EMBL:X06958; NID:94374; PIDN:CAA30028.1; PID:g4375
R:Newton, C.H.; Shimmin, L.C.; Yes, J.; Dennis, P.P.
J. Bacteriol. 172, 579-588, 1990
A:Title: A family of genes encode the multiple forms of the Saccharomyces cerevisiae rib
1 protein.
A:Reference number: A35109; MUID:90130289; PMID:2404943
A:Accession: B35109
A:Molecule type: DNA
A:Residues: 1-106 <NEW>
A:Cross-references: GB:M26503; NID:gl71816; PIDN:AAA34735.1; PID:gl71817
R:Habbig, B.; Hattenhorst, U.; Hollenberg, C.P.; Ramezani Rad, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66703
A:Accession: S66722
A:Molecule type: DNA
A:Residues: 1-106 <HAB>
A:Cross-references: EMBL:Z74781; NID:gl419834; PIDN:CAA99041.1; PID:gl419835; GSPDB:GN000
A:Experimental source: strain S288C
R:Ansong, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wienann, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66723
A:Accession: S66724
A:Molecule type: DNA
```

```
C90225
hypothetical protein SS06469 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: C90225
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90225
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813934; PIDN:AAK41058.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS06469

Query Match 3.6%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 MPRPGYK 81
DB 1 MPRPGYK 7

RESULT 7
A:2413
Hypothetical protein asl4865 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: A12413
R:Kikuno, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12413
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA876564.1; PID:gl7134002; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl4865

Query Match 3.6%; Score 7; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 YFLGLKV 97
DB 54 YFLGLKV 60

RESULT 6
C90225
hypothetical protein SS06469 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: C90225
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90225
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813934; PIDN:AAK41058.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS06469

Query Match 3.6%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 MPRPGYK 81
DB 1 MPRPGYK 7

RESULT 7
```

A;Residues: 1-106 <ANS>  
A;Cross-references: EMBL:274781; NID:gl1419834; PIDN:CAA99041.1; PID:gl1419835; GSPDB:GN00  
A;Experimental source: strain S28C  
R;Santos, C.; Ortiz-Reyes, B.; Naranda, T.; Remacha, M.; Ballesta, J.P.G.  
Biochemistry 32, 4231-4236, 1993  
A;Title: The acidic phosphoproteins from Saccharomyces cerevisiae ribosomes. NH-2-termin  
A;Reference number: A49495; MUID:93237229; PMID:8476850  
A;Accession: A49495  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <SAN>  
C;Genetics:  
A;Gene: SGD:RPLA2; RPA2; MIPS:YOL039W  
A;Cross-references: SGD:S0005399; MIPS:YOL039W  
A;Map position: 15L  
C;Superfamily: rat acidic ribosomal protein P1  
C;Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 3.6%; Score 7; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AEEKEE 193  
DB 84 AEEKEE 90

RESULT 9  
R8BY2B  
acidic ribosomal protein P1.e.B, cytosolic - yeast (Saccharomyces cerevisiae)  
N;Alternate names: acidic ribosomal protein P1.beta; protein YDL130w; rib  
C;Species: Saccharomyces cerevisiae  
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 21-Jul-2000  
C;Accession: C28104; D35109; C49495; B49495; S67673  
R;Remacha, M.; Saenz-Robles, M.T.; Vilella, M.D.; Ballesta, J.P.G.  
J. Biol. Chem. 263, 9094-9101, 1998  
A;Title: Independent genes coding for three acidic proteins of the large ribosomal subun  
A;Reference number: A92726; MUID:88243786; PMID:2837476  
A;Accession: C28104  
A;Molecule type: DNA  
A;Residues: 1-106 <REM>  
A;Cross-references: EMBL:M19238; NID:gl172399; PIDN:AAA34973.1; PID:gl172400  
R;Newton, C.H.; Shimmin, L.C.; Yee, J.; Dennis, P.P.  
J. Bacteriol. 172, 579-588, 1990  
A;Title: A family of genes encode the multiple forms of the Saccharomyces cerevisiae rib  
1 protein.  
A;Reference number: A35109; MUID:90130289; PMID:2404943  
A;Accession: D35109  
A;Molecule type: DNA  
A;Residues: 1-106 <NEW>  
A;Cross-references: EMBL:M26507; NID:gl171814; PIDN:AAA34734.1; PID:gl171815  
R;Santos, C.; Ortiz-Reyes, B.; Naranda, T.; Remacha, M.; Ballesta, J.P.G.  
Biochemistry 32, 4231-4236, 1993  
A;Title: The acidic phosphoproteins from Saccharomyces cerevisiae ribosomes. NH-2-termin  
A;Reference number: A49495; MUID:93237229; PMID:8476850  
A;Accession: C49495  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 9-16 <SAN>  
A;Accession: B49495  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 2-5 <SAW>  
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.; Wagner, G.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67655  
A;Accession: S67673  
A;Molecule type: DNA  
A;Residues: 1-106 <RIB>  
A;Cross-references: EMBL:Z74178; NID:gl1431196; PIDN:CAA98698.1; PID:gl1431197; GSPDB:GN00  
A;Experimental source: strain S28C  
C;Genetics:  
A;Gene: SGD:RPLA3; RPL44; MIPS:YDL130W

A;Cross-references: SGD:S0002288; MIPS:YDL130W  
A;Map position: 4L  
A;Introns: 38/3  
C;Superfamily: rat acidic ribosomal protein P1  
C;Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 3.6%; Score 7; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AEEKEE 193  
DB 84 AEEKEE 90

RESULT 10  
T2147  
ribosomal protein rplal [imported] - yeast (Candida albicans)  
C;Species: Candida albicans  
C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 03-Nov-2000  
C;Accession: T52147  
R;Taylor, K.; Harris, D.  
submitted to the EMBL Data Library, November 1998  
A;Reference number: Z25985  
A;Accession: T52147  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-106 <TAY>  
A;Cross-references: EMBL:AL033497; PIDN:CAA21967.1  
A;Experimental source: strain 1161; Cosmid Ca49C10  
C;Genetics:  
A;Gene: rplal  
A;Map position: 1  
C;Superfamily: rat acidic ribosomal protein P1  
C;Keywords: protein biosynthesis; ribosome

Query Match 3.6%; Score 7; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AEEKEE 193  
DB 84 AEEKEE 90

RESULT 11  
R5BYA1  
acidic ribosomal protein P2.e.B, cytosolic - yeast (Saccharomyces cerevisiae)  
N;Alternate names: acidic ribosomal protein P2.alpha; protein YDR382w; 1  
C;Species: Saccharomyces cerevisiae  
C;Date: 31-Oct-1980 #sequence\_revision 31-Mar-1992 #text\_change 21-Jul-2000  
C;Accession: A35109; A28104; A02776; S61177; S69666  
R;Newton, C.H.; Shimmin, L.C.; Yee, J.; Dennis, P.P.  
J. Bacteriol. 172, 579-588, 1990  
A;Title: A family of genes encode the multiple forms of the Saccharomyces cerevisiae rib  
1 protein.  
A;Reference number: A35109; MUID:90130289; PMID:2404943  
A;Accession: A35109  
A;Molecule type: DNA  
A;Residues: 1-110 <NEW>  
A;Cross-references: GB:M26505; NID:gl171810; PIDN:AAA34732.1; PID:gl171811  
R;Remacha, M.; Saenz-Robles, M.T.; Vilella, M.D.; Ballesta, J.P.G.  
J. Biol. Chem. 263, 9094-9101, 1998  
A;Title: Independent genes coding for three acidic proteins of the large ribosomal subuni  
A;Reference number: A92726; MUID:88243786; PMID:2837476  
A;Accession: A28104  
A;Molecule type: DNA  
A;Residues: 1-110 <REM>  
A;Cross-references: EMBL:J03761; NID:gl172397; PIDN:AAA34972.1; PID:gl172398  
A;Note: the authors translated the codon GAA for residue 28 as Ala  
R;Itch, T.  
Biochim. Biophys. Acta 671, 16-24, 1981  
A;Title: Primary structure of an acidic ribosomal protein YPA1 from Saccharomyces cerevis

A:Reference number: A02776; MUID:82069169; PMID:7030402  
A:Accession: A02776  
A:Molecule type: protein  
A:Residues: 1-74, 'GPAS', 79-85, 'G', 86-90, 92-110 <ITO>  
R: Ding, H.  
Submitted to the EMBL Data Library, June 1995  
A:Description: The sequence of *S. cerevisiae* cosmid 9481.  
A:Reference number: S61159  
A:Accession: S61177  
A:Molecule type: DNA  
A:Residues: 1-110 <DIN>  
A:Cross-references: EMBL:U28373; NID:G849184; PIDN:AAB64818.1; PID:G849203; GSPDB:GN000000  
A:Experimental source: strain S288C (AB972)  
R: Dietrich, F.S.  
Submitted to the EMBL Data Library, July 1995  
A:Description: The sequence of *S. cerevisiae* cosmids 9481, 9509, 9926, 9461, and lambda  
A:Reference number: S69665  
A:Accession: S69666  
A:Molecule type: DNA  
A:Residues: 1-110 <DIE>  
A:Cross-references: EMBL:U32274; NID:G927313; PIDN:AAB64824.1; PID:G927315; GSPDB:GN000000  
C:Genetics:  
A:Gene: SGD:RPL45; RPL44; MIPS:YDR382\*  
A:Cross-references: SGD:S0002790; MIPS:YDR382W  
A:Map position: 4R  
C:Superfamily: rat acidic ribosomal protein P1  
C:Keywords: phosphoprotein; protein biosynthesis; ribosome  
F:1-110/Product: acidic ribosomal protein P2.e.B #status experimental <MAT>  
  
Query Match 3.6%; Score 7; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 187 ABEKEE 193  
DB 88 ABEKEE 94  
|||||  
RESULT 12  
S43115  
acidic ribosomal protein P2 - fungus (Cladosporium herbarum)  
C:Species: Cladosporium herbarum  
C:Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 13-Aug-1999  
A:Accession: S43115  
R: Achatz, G.; Oberkofler, H.; Simon, B.; Lechenauer, E.; Unger, A.; Kandler, D.; Prillinger, A.  
Submitted to the EMBL Data Library, March 1994  
A:Description: Molecular characterization of allergens of Cladosporium herbarum and Alternaria  
A:Reference number: S43108  
A:Accession: S43115  
A:Molecule type: mRNA  
A:Residues: 1-111 <ACH>  
A:Cross-references: EMBL:X78223; NID:G467626; PIDN:CAA55067.1; PID:G467627  
C:Superfamily: rat acidic ribosomal protein P1  
  
Query Match 3.6%; Score 7; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 187 ABEKEE 193  
DB 94 ABEKEE 100  
|||||  
RESULT 13  
T01132  
cyclin-dependent kinase inhibitor protein [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F26B6.8  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 16-Feb-2001  
A:Accession: T01132; F46424  
R: Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, A.  
Submitted to the EMBL Data Library, June 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.  
  
A:Reference number: Z14198  
A:Accession: T01132  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-191 <ROU>  
A:Cross-references: EMBL:AC003040; NID:G3242700; PID:G3242706  
A:Experimental source: cultivar Columbia  
R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; A. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083497; PMID:10617197  
A:Accession: F84624  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-191 <STO>  
A:Cross-references: GB:AE002093; NID:G3242706; PIDN:AAC23758.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: F26B6.8; At2g23430  
A:Map position: 2  
A:Introns: 66/3; 81/2; 170/2  
  
Query Match 3.6%; Score 7; DB 2; Length 191;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 188 EEEKEE 194  
DB 93 EEEKEE 99  
|||||  
RESULT 14  
S34144  
lipase - Serratia proteamaculans  
C:Species: Serratia proteamaculans  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
A:Accession: S34144  
R: Smigielski, A.J.; Zhang, Q.; Akhurst, R.J.  
Submitted to the EMBL Data Library, January 1993  
A:Description: nucleotide sequence of a lipase gene isolated from Serratia proteamaculans  
A:Reference number: S34144  
A:Accession: S34144  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <SMI>  
A:Cross-references: EMBL:Z19596; NID:G313122; PIDN:CAA79652.1; PID:G313123  
  
Query Match 3.6%; Score 7; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 SLGGGLA 19  
DB 132 SLGGGLA 138  
|||||  
RESULT 15  
T29685  
hypothetical protein F39F10.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
A:Accession: T29685  
R: Stellyes, L.; Gattung, S.  
Submitted to the EMBL Data Library, May 1996  
A:Description: The sequence of *C. elegans* cosmid F39F10.  
A:Reference number: Z20664  
A:Accession: T29685  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <STB>  
A:Cross-references: EMBL:U58743; PIDN:AAB00614.1; GSPDB:GN00028; CESP:F39F10.2  
A:Experimental source: strain Bristol N2; clone F39F10

C:Genetics:  
A:Gene: CESP:F39F10.2  
A:Map position: X  
A:Introns: 85/1; 146/3; 231/3  
C:Superfamily: Kinase-related transforming protein; protein kinase homology

Query Match 3.6%; Score 7; DB 2; Length 298;  
Best Local Similarity 100.0%; Fred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SLGGGLA 19  
|||  
Db 276 SLGGGLA 282

Search completed: May 17, 2004, 10:53:16  
Job time : 44 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:47:35 ; Search time 18 Seconds  
(without alignments)  
561.201 Million cell updates/sec

Title: US-10-621-401-145  
Perfect score: 194  
Sequence: 1 MKLASGFLVWLSSGGGLAQ.....PFMNSQRAACICABEKEEL 194

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	70.6	195	1 PA2Z HUMAN	Q9bx93 homo sapien
2	38	19.6	195	1 PA2Z MOUSE	Q99p27 mus musculus
3	8	4.1	214	1 ADEN ADRA1	P11826 human adeno
4	7	3.6	106	1 RLA2 YEAST	P05319 saccharomyc
5	7	3.6	106	1 RLA3 YEAST	P10622 saccharomyc
6	7	3.6	110	1 RLA4 CLAEH	P50344 cladosporiu
7	7	3.6	110	1 RLA4 YEAST	P02400 saccharomyc
8	7	3.6	111	1 RLA4 CLAEH	P42039 cladosporiu
9	7	3.6	204	1 TD53 HUMAN	Q16890 homo sapien
10	7	3.6	204	1 TD53 MOUSE	Q54818 mus musculus
11	7	3.6	210	1 TD53 CHICK	Q91864 gallus gall
12	7	3.6	319	1 PA1 SERLI	P18952 serratia li
13	7	3.6	338	1 RLA0 METJA	P54049 methanococc
14	7	3.6	420	1 MSME STRMU	Q00749 streptococc
15	7	3.6	434	1 CBPH BOVIN	P04836 bos taurus
16	7	3.6	476	1 CBPH HUMAN	P16870 homo sapien
17	7	3.6	476	1 CBPH MOUSE	Q00493 mus musculus
18	7	3.6	476	1 CBPH RAT	P15087 rattus norv
19	7	3.6	557	1 CAB1 AQAAE	Q67869 aquifex aeo
20	7	3.6	585	1 SAC1 CHLRE	Q39593 chlamydomon
21	7	3.6	649	1 S281 HUMAN	Q00337 homo sapien
22	7	3.6	875	1 ARS2 MOUSE	Q99mr6 mus musculus
23	7	3.6	875	1 ARS2 HUMAN	Q9bpx5 homo sapien
24	7	3.6	1083	1 MAN1 YEAST	P22855 saccharomyc
25	7	3.6	1135	1 RPC2 DROME	P25167 drosophila
26	7	3.6	1191	1 SMC3 RAT	P97690 rattus norv
27	7	3.6	1217	1 SMC3 HUMAN	Q9uq77 homo sapien
28	7	3.6	1217	1 SMC3 MOUSE	Q9cwo3 mus musculus
29	7	3.6	1218	1 SMC3 BOVIN	Q97594 bos taurus
30	7	3.6	1387	1 RGSC RAT	Q08774 rattus norv
31	7	3.6	4725	1 DYHC DICDI	P34036 dictyosteli
32	6	3.1	68	1 YN40 THETN	Q9r7q8 thermoanaer
33	6	3.1	70	1 UBIL_CABER	Q07371 caenorhabdi

34	6	3.1	70	1	UBIL_CAEEL	Q07372 caenorhabdi
35	6	3.1	74	1	Y350 METKA	Q8tyf0 methanopyru
36	6	3.1	89	1	BAF_HUMAN	Q75531 homo sapien
37	6	3.1	89	1	BAF_MOUSE	Q54962 mus musculus
38	6	3.1	89	1	BAF_RAT	Q9xlt1 rattus norv
39	6	3.1	100	1	NUOK_BUCBP	Q89at7 buchnera ap
40	6	3.1	102	1	LE19 GOSHI	P09443 gossypium h
41	6	3.1	107	1	RL12 PYRAB	Q9uxs6 pyrococcus
42	6	3.1	108	1	HX8 RAT	P18866 rattus norv
43	6	3.1	108	1	RL12 PYRHO	Q57705 pyrococcus
44	6	3.1	110	1	RLA1_ALTAL	P49148 alternaria
45	6	3.1	111	1	RL23 CHLMU	Q9pjl6 chlamydia m
46	6	3.1	111	1	RLA2 ASPFU	Q9uuz6 aspergillus
47	6	3.1	111	1	RLA3 CLAEH	P42038 cladosporiu
48	6	3.1	113	1	RK20 CVAPA	P14809 cyanophora
49	6	3.1	113	1	RLA2 ALTAL	P42037 alternaria
50	6	3.1	115	1	RK20 CVACA	Q9t1s0 cyanidium c
51	6	3.1	119	1	RLA3 MAIZE	Q24413 zea mays (m
52	6	3.1	122	1	YU2C BACSU	Q32089 bacillus su
53	6	3.1	127	1	YCBK HAEIN	P44284 haemophilus
54	6	3.1	128	1	Y280 METJA	Q57728 methanococc
55	6	3.1	151	1	YBRJ_ECOLI	P75709 escherichia
56	6	3.1	152	1	PSAL CVACA	Q9tln7 cyanidium c
57	6	3.1	167	1	YDAE BACSU	P96578 bacillus su
58	6	3.1	171	1	CFLA HSVE2	Q66674 equine herp
59	6	3.1	171	1	GCS4 AQAAE	Q67192 aquifex aeo
60	6	3.1	173	1	NU6M GADMO	P55783 gadus morhu
61	6	3.1	176	1	AROK MYCTU	P95014 mycobacteri
62	6	3.1	182	1	MCRC METVO	P11567 methanococc
63	6	3.1	186	1	FREQ DROME	P37236 drosophila
64	6	3.1	189	1	PA2Y HUMAN	Q9bami homo sapien
65	6	3.1	191	1	RNMC MONCH	P23540 momordica c
66	6	3.1	192	1	PA2Y MOUSE	Q9ep12 mus musculus
67	6	3.1	196	1	IF3 WIGHR	Q8d3b9 wigleswort
68	6	3.1	198	1	MCRC METVA	P07960 methanococc
69	6	3.1	200	1	MCRC METJA	Q58254 methanococc
70	6	3.1	202	1	RUVA PSESM	Q87y34 pseudomonas
71	6	3.1	203	1	RUVA ECOLI	P08576 escherichia
72	6	3.1	203	1	RUVA SALTY	Q8xth9 salmonella
73	6	3.1	204	1	RUVA YERPE	Q8zeu6 yersinia pe
74	6	3.1	205	1	RUVA PSEPK	Q88j11 pseudomonas
75	6	3.1	206	1	MCRC METBA	P07959 methanocarc
76	6	3.1	211	1	RCNI YEAST	P36054 saccharomyc
77	6	3.1	213	1	NEUM CARAU	P17691 carassius a
78	6	3.1	221	1	CFI PHAVU	P14238 phaseolus v
79	6	3.1	222	1	ERF4 ARATH	Q80340 arabidopsis
80	6	3.1	224	1	CFI_PUELO	Q43056 pueraria lo
81	6	3.1	226	1	NEUM RAT	P07936 rattus norv
82	6	3.1	228	1	NEUA HAEIN	Q57140 haemophilus
83	6	3.1	232	1	PSD RHIL0	Q984w0 rhizobium l
84	6	3.1	232	1	YK10 ARCFU	Q28269 archaeoglob
85	6	3.1	234	1	SPEG STRPY	Q9x5c7 streptococc
86	6	3.1	239	1	3MGH_PSEAE	Q9hx17 pseudomonas
87	6	3.1	239	1	AXIC ARATH	Q38810 arabidopsis
88	6	3.1	239	1	GIDB CLOTE	Q89980 clostridium
89	6	3.1	242	1	HCX8 HUMAN	P31273 homo sapien
90	6	3.1	242	1	HCX8 MOUSE	P09025 mus musculus
91	6	3.1	243	1	TRMD BACSU	Q31741 bacillus su
92	6	3.1	247	1	AXID ARATH	Q38831 arabidopsis
93	6	3.1	252	1	TPIS_LACPL	Q88yh4 lactobacill
94	6	3.1	256	1	PYRK STRR6	Q8dq38 streptococc
95	6	3.1	258	1	FLIR AQAAE	Q67773 aquifex aeo
96	6	3.1	259	1	YG47 SYN3	P74369 synechocyst
97	6	3.1	260	1	THI4 METAC	Q8tm19 methanosarc
98	6	3.1	260	1	THI4 METMA	Q8qb55 methanosarc
99	6	3.1	262	1	Y096 METJA	Q57561 methanococc
100	6	3.1	279	1	CTCI HUMAN	Q9btx7 homo sapien
101	6	3.1	280	1	THTM ECO57	P58388 escherichia
102	6	3.1	280	1	THTM ECOLI	P31142 escherichia
103	6	3.1	281	1	RP32 HAEIN	P44404 haemophilus
104	6	3.1	282	1	YFHH_ECOLI	P37767 escherichia
105	6	3.1	283	1	BRUI_SOYBN	P35694 glycine max
106	6	3.1	284	1	DAPF_BUCAI	P57649 buchnera ap



107	6	3.1	284	1	POLG_PVYVO	P11897	potato viru	180	6	3.1	421	1	EXOF_RHIME	Q02728	rhizobium m
108	6	3.1	284	1	RP32_PROMI	P50509	proteus mir	181	6	3.1	421	1	PGK_EMENI	P11977	emeritella
109	6	3.1	285	1	RP32_ENTCL	P50508	enterobacte	182	6	3.1	421	1	SYH_CORSU	Q83c80	coxiella bu
110	6	3.1	289	1	RL15_ARATH	Q38911	arabidopsis	183	6	3.1	422	1	PAN1_HUMAN	Q14653	homo sapien
111	6	3.1	290	1	ILVE_RICCN	Q92126	rickettsia	184	6	3.1	427	1	IRF3_HUMAN	Q14653	homo sapien
112	6	3.1	290	1	ILVE_RICPR	O05970	rickettsia	185	6	3.1	427	1	YF05_MEITH	O27549	methanobact
113	6	3.1	291	1	CHIA_TOBAC	P20960	nicotiana t	186	6	3.1	427	1	YKTS_YEAST	P36046	saccharomyc
114	6	3.1	291	1	CHIA_ARATH	O81958	arabidopsis	187	6	3.1	428	1	PUR2_SALTI	Q73434	salmonella
115	6	3.1	293	1	CHIA_CICAR	P36908	cicer ariet	188	6	3.1	429	1	PUR2_SALTY	P26977	salmonella
116	6	3.1	293	1	ACTR_SHEEP	Q91077	ovis aries	189	6	3.1	429	1	MURD_THEMA	Q8976	thermotoga
117	6	3.1	295	1	ACTR_MOUSE	Q64326	mus musculu	190	6	3.1	430	1	TOLB_YERPE	O8976	thermotoga
118	6	3.1	296	1	VG21_HSV11	Q00114	ictaluriid h	191	6	3.1	430	1	AK_CHLTR	O84367	chlamydia t
119	6	3.1	297	1	ACTR_BOVIN	P34974	bos taurus	192	6	3.1	431	1	KKQ1_YEAST	P36005	saccharomyc
120	6	3.1	298	1	REM_HUMAN	O75628	homo sapien	193	6	3.1	433	1	SYH_BORER	Q7467	bordetella
121	6	3.1	302	1	CHIA_ARATH	P19172	arabidopsis	194	6	3.1	434	1	SYH_BORFE	Q7467	bordetella
122	6	3.1	310	1	KITH_HSVTF	P13157	turkey herp	195	6	3.1	434	1	RBL1_ARCFU	O28685	archaeoglob
123	6	3.1	311	1	CHLY_HEVER	P23472	hevea bras	196	6	3.1	437	1	ARP6_YEAST	P32509	saccharomyc
124	6	3.1	313	1	RLA0_NEUCR	Q96tj5	neurospora	197	6	3.1	438	1	PPAS_MOUSE	P35396	mus musculu
125	6	3.1	320	1	Y678_METJA	P53156	saccharomyc	198	6	3.1	440	1	PPAS_MOUSE	Q03181	homo sapien
126	6	3.1	320	1	Y678_METJA	Q89gnl	homo sapien	199	6	3.1	441	1	G6PI_MYCSM	P96803	mycobacteri
127	6	3.1	323	1	O6T1_HUMAN	P77969	synecocyst	200	6	3.1	442	1	G6PI_MYCSM	P45627	lactobacill
128	6	3.1	327	1	HEM2_SYNY3	O67876	aquifex aeo	201	6	3.1	445	1	GLNA_LACDE	P22013	colletotric
129	6	3.1	330	1	HEM2_AQUAE	Q98g36	mycoplasma	202	6	3.1	445	1	THB1_COLGR	O62729	canis famli
130	6	3.1	330	1	RS2_MYCPU	P46860	escherichia	203	6	3.1	446	1	NY5R_CANFA	O97969	sus scrofa
131	6	3.1	331	1	GNTF_ECOLI	O81zul	homo sapien	204	6	3.1	446	1	NY5R_PIG	P19577	bacteroides
132	6	3.1	332	1	PASA_HUMAN	Q28944	homo sapien	205	6	3.1	448	1	PRTE_BACNO	Q15761	homo sapien
133	6	3.1	334	1	CATL_PIG	Q60178	methanococc	206	6	3.1	455	1	NY5R_HUMAN	Q63634	rattus norv
134	6	3.1	335	1	HEM2_METJA	P37055	escherichia	207	6	3.1	456	1	NY5R_RAT	P05306	bacillus su
135	6	3.1	337	1	HNR_ECOLI	O52705	methanococc	208	6	3.1	460	1	PTSB_BAGSU	P77793	escherichia
136	6	3.1	338	1	RLA0_METTL	O28781	archaeoglob	209	6	3.1	460	1	YDDV_ECOLI	P52276	synecocyst
137	6	3.1	339	1	RLA0_ARCTU	Q48759	listeria mo	210	6	3.1	462	1	SYN_SYNY3	Q935y7	synecocyst
138	6	3.1	340	1	Y231_LISMO	Q92f44	listeria in	211	6	3.1	465	1	GLGA_SYN7	P10354	rattus norv
139	6	3.1	340	1	Y263_ECOLI	P06964	escherichia	212	6	3.1	466	1	CMGA_RAT	O70342	mus musculu
140	6	3.1	341	1	CYTR_ECOLI	P74438	synecocyst	213	6	3.1	466	1	NY5R_MOUSE	P39900	homo sapien
141	6	3.1	342	1	PYRC_SYNY3	O74109	pyrococcus	214	6	3.1	470	1	MM12_HUMAN	Q89yq9	anabaena sp
142	6	3.1	342	1	RLA0_PVRHO	P37190	escherichia	215	6	3.1	471	1	TIG_ANASP	Q28397	equus cabal
143	6	3.1	346	1	GATD_ECOLI	Q8vg23	bartonella	216	6	3.1	477	1	MM03_HORSE	P56517	gallus gall
144	6	3.1	348	1	LPXD_BARHE	Q58542	methanococc	217	6	3.1	480	1	HDAL_CHICK	P11914	saccharomyc
145	6	3.1	349	1	ARSA_METJA	P25987	turkey herp	218	6	3.1	482	1	MPPA_YEAST	Q00772	saccharomyc
146	6	3.1	350	1	KITH_HSVTU	Q9c1r9	lactococcus	219	6	3.1	484	1	SLT2_YEAST	Q00270	hepatitis e
147	6	3.1	352	1	ADD_LACIA	Q98019	sulfolobus	220	6	3.1	485	1	SECY_CYAPA	P25014	cyanophora
148	6	3.1	354	1	AROB_SULSO	Q9bdk6	sus scrofa	221	6	3.1	492	1	TYTR_TRYBB	P39051	trypanosoma
149	6	3.1	355	1	ATNE_PIG	Q9un42	homo sapien	222	6	3.1	492	1	TYTR_TRYBB	P28593	trypanosoma
150	6	3.1	357	1	ATNE_HUMAN	Q10717	zea mays	223	6	3.1	494	1	HMBC_DROME	P09081	drosophila
151	6	3.1	360	1	CYS2_MAIZE	P51173	dictyosteli	224	6	3.1	494	1	SYE_PSEAE	Q9xcl6	pseudomonas
152	6	3.1	361	1	APEA_DICDI	P73997	synecocyst	225	6	3.1	500	1	XNBE_THESA	P36906	thermoanaer
153	6	3.1	361	1	AROB_SYNY3	Q9axe3	daucus caro	226	6	3.1	500	1	XNBE_THESJ	O30360	thermoanaer
154	6	3.1	361	1	DCAM_DAUCA	P05167	hordeum vul	227	6	3.1	501	1	MKC1_CANAL	P43068	candida alb
155	6	3.1	362	1	ALEU_HORVU	Q96555	datura stra	228	6	3.1	501	1	PLI3_ARATH	Q93204	arabidopsis
156	6	3.1	362	1	DCAM_DATST	Q96555	datura stra	229	6	3.1	502	1	C718_MENPI	Q42716	mentha pipe
157	6	3.1	363	1	ENGC_XANAC	Q89pw9	xanthomonas	230	6	3.1	502	1	HKX2_ARATH	P93834	arabidopsis
158	6	3.1	371	1	PA6B_MOUSE	Q9jR83	mus musculu	231	6	3.1	503	1	LCYB_NARPS	Q40424	narcissus p
159	6	3.1	372	1	PA6B_HUMAN	Q9by95	homo sapien	232	6	3.1	504	1	FLIC_SALMO	Q08973	salmonella
160	6	3.1	376	1	MED7_SCHPO	O60104	schizosacch	233	6	3.1	504	1	FLIC_SALMO	Q08968	salmonella
161	6	3.1	376	1	P33_MYCPE	Q50368	mycoplasma	234	6	3.1	507	1	FLIC_SALMO	Q06974	salmonella
162	6	3.1	380	1	LE22_PVRAB	Q9v1j0	pyrococcus	235	6	3.1	511	1	TRPE_STRCO	Q944w7	streptomyce
163	6	3.1	384	1	PRM1_TRIAL	P06873	tritirachiu	236	6	3.1	512	1	GUAA_THETN	Q8rc63	thermoanaer
164	6	3.1	388	1	RIMT_MOUSE	Q99ne5	mus musculu	237	6	3.1	514	1	CP24_HUMAN	Q07973	homo sapien
165	6	3.1	390	1	ARGD_METTH	O27392	methanobact	238	6	3.1	514	1	SYB_METMP	O30520	methanococc
166	6	3.1	394	1	CEGT_HUMAN	Q16739	homo sapien	239	6	3.1	523	1	PUR9_STRCO	Q9ky50	s bifunctio
167	6	3.1	395	1	CRTC_CAEOL	P27798	caenorhabdi	240	6	3.1	524	1	TXN2_HUMAN	Q9nnw7	homo sapien
168	6	3.1	399	1	PNCB_ECO57	Q8x8e8	escherichia	241	6	3.1	525	1	WVIN_VIBCH	O34238	vibrio chol
169	6	3.1	399	1	PNCB_ECOLI	P18133	escherichia	242	6	3.1	525	1	WVIN_VIBCH	P04849	simian viru
170	6	3.1	403	1	SYH_AQUAE	Q66522	aquifex aeo	243	6	3.1	529	1	VGLF_SV5	Q8bg30	mus musculu
171	6	3.1	406	1	PKD3_HUMAN	Q15120	homo sapien	244	6	3.1	530	1	NLFA_MOUSE	P31549	escherichia
172	6	3.1	412	1	TGF3_CHICK	P16047	gallus gall	245	6	3.1	536	1	THIP_ECOLI	Q16c10	homo sapien
173	6	3.1	414	1	NSR1_YEAST	P27476	saccharomyc	246	6	3.1	540	1	ECM1_HUMAN	Q8k2w9	mus musculu
174	6	3.1	414	1	YOJL_BACSU	O31852	bacillus su	247	6	3.1	541	1	CN93_MOUSE	Q9y466	aeropyrum p
175	6	3.1	416	1	PGK_AGRAB	Q94123	agaricus bi	248	6	3.1	548	1	THSB_AERPE	Q9h3p2	homo sapien
176	6	3.1	417	1	PGK_ASPOR	P41756	aspergillus	249	6	3.1	549	1	NLFA_HUMAN	P38799	saccharomyc
177	6	3.1	418	1	EF1G_ORYSA	Q9zri7	oryza sativ	250	6	3.1	552	1	YHN8_YEAST	Q02916	coturnix co
178	6	3.1	419	1	CMLA_PSEAE	P32482	pseudomonas	251	6	3.1	555	1	NFL_COTJA	Q02916	coturnix co
179	6	3.1	420	1	PR11_HUMAN	P49642	homo sapien	252	6	3.1	556	1	HIR3_HUMAN	Q9bw71	homo sapien

253	1	558	3.1	6	326	798	1	FBL1_CAEEL	077469 caenorhabdi
254	1	560	3.1	6	327	805	1	IF2_AQUAE	067825 aquifex aeo
255	1	562	3.1	6	328	811	1	SYG_SCHPO	Q9Y7Y8 schizosacch
256	1	572	3.1	6	329	841	1	IEG3_MCMVS	Q69154 murine cyto
257	1	574	3.1	6	330	855	1	RDJ5_ARATH	Q8W3J8 arabidopsis
258	1	575	3.1	6	331	857	1	NFM_CHICK	P16053 gallus gall
259	1	577	3.1	6	332	860	1	CHT2_COCPO	P54197 coccidioid
260	1	578	3.1	6	333	864	1	LOX2_PEA	P14856 pisum sativ
261	1	583	3.1	6	334	866	1	MYSP_SCHJA	Q05870 schistosoma
262	1	590	3.1	6	335	866	1	MYSP_SCHMA	Q06198 schistosoma
263	1	591	3.1	6	336	875	1	UBP7_SCHPO	Q9P7E5 schizosacch
264	1	592	3.1	6	337	881	1	SYA_CLOAB	Q97193 clostridium
265	1	592	3.1	6	338	882	1	DIS1_SCHPO	Q09933 schizosacch
266	1	593	3.1	6	339	882	1	RA50_PYRPU	P58301 pyrococcus
267	1	600	3.1	6	340	885	1	RPA1_THEAC	Q03585 thermoplas
268	1	603	3.1	6	341	894	1	MPRA_BACSU	P54423 bacillus su
269	1	609	3.1	6	342	897	1	SAP1_YEAST	P39955 saccharomyc
270	1	613	3.1	6	343	901	1	ACON_STAAM	Q99UC8 staphylococ
271	1	614	3.1	6	344	901	1	ACON_STAEP	Q8CP22 staphylococ
272	1	614	3.1	6	345	908	1	ACON_BACSU	P09339 bacillus su
273	1	618	3.1	6	346	908	1	DPO1_BORBU	O51498 borrelia bu
274	1	619	3.1	6	347	912	1	PGCB_BOVIN	Q28062 bos taurus
275	1	621	3.1	6	348	947	1	PODK_MAIZE	P11155 zea mays (m
276	1	621	3.1	6	350	949	1	AHM6_ARATH	Q28029 arabidopsis
277	1	621	3.1	6	351	950	1	GYP2_YEAST	P53358 saccharomyc
278	1	627	3.1	6	352	954	1	K6P1_YARLI	P59680 yarrowia li
279	1	627	3.1	6	353	970	1	AND1_MOUSE	P59328 mus musculu
280	1	629	3.1	6	354	974	1	POD1_CAUCR	Q92988 caulobacter
281	1	632	3.1	6	355	974	1	VIL4_ARATH	O65570 arabidopsis
282	1	634	3.1	6	356	979	1	UB37_HUMAN	Q86582 homo sapien
283	1	636	3.1	6	357	996	1	NPH1_ARATH	O48963 arabidopsis
284	1	639	3.1	6	358	1003	1	SYG_CHLMU	Q9PC66 chlamydia m
285	1	644	3.1	6	359	1003	1	SYG_CHLTR	O46371 chlamydia t
286	1	646	3.1	6	360	1016	1	DPO1_RHILE	O9SLQ2 rhizobium l
287	1	647	3.1	6	361	1017	1	EM11_MOUSE	Q99K41 mus musculu
288	1	657	3.1	6	362	1021	1	SECA_ARATH	Q98Y10 arabidopsis
289	1	657	3.1	6	363	1025	1	MK21_YEAST	Q12176 saccharomyc
290	1	659	3.1	6	364	1031	1	YDG9_SCHPO	Q10496 schizosacch
291	1	659	3.1	6	365	1036	1	SECA_SPIOL	Q36795 spinacia ol
292	1	660	3.1	6	366	1048	1	P100_HCMVA	P08318 human cytom
293	1	660	3.1	6	367	1049	1	RDJ6_ARATH	Q94HW3 arabidopsis
294	1	660	3.1	6	368	1051	1	ULK1_MOUSE	O70405 mus musculu
295	1	666	3.1	6	369	1059	1	POL2_DROME	P20825 drosophila
296	1	668	3.1	6	370	1065	1	DP3A_STAEP	O8CWX0 staphylococ
297	1	680	3.1	6	371	1066	1	AOSL_PLEHO	O16025 plexaura ho
298	1	688	3.1	6	372	1073	1	MTR4_YEAST	P47047 saccharomyc
299	1	690	3.1	6	373	1083	1	KCH3_HUMAN	Q9UL86 homo sapien
300	1	705	3.1	6	374	1087	1	KCH3_MOUSE	Q9WV10 mus musculu
301	1	708	3.1	6	375	1087	1	KCH3_RAT	O89047 rattus norv
302	1	709	3.1	6	376	1112	1	RAL3_SCHPO	P28706 schizosacch
303	1	728	3.1	6	377	1132	1	TERT_HUMAN	O14746 homo sapien
304	1	732	3.1	6	378	1150	1	S126_HUMAN	Q9UHW9 homo sapien
305	1	733	3.1	6	379	1150	1	S126_MOUSE	Q924N4 mus musculu
306	1	735	3.1	6	380	1186	1	DNBI_HSVB2	P12639 bovine herp
307	1	735	3.1	6	381	1192	1	KZ_DROME	O46072 drosophila
308	1	735	3.1	6	382	1196	1	DNBI_HSV2H	P89452 herpes simp
309	1	736	3.1	6	383	1197	1	DNBI_HSV2	P36384 herpes simp
310	1	737	3.1	6	384	1233	1	B3A3_RABIT	O18917 oryctolagus
311	1	748	3.1	6	385	1247	1	SAH1_HUMAN	O94885 homo sapien
312	1	752	3.1	6	386	1257	1	PER2_MOUSE	O54943 mus musculu
313	1	754	3.1	6	387	1257	1	RBB1_HUMAN	P29374 homo sapien
314	1	755	3.1	6	388	1290	1	RPOC_MYCPN	P75271 mycoplasma
315	1	756	3.1	6	389	1337	1	PAD3_RAT	Q92340 rattus norv
316	1	758	3.1	6	390	1356	1	PAD3_HUMAN	Q8TEW0 homo sapien
317	1	775	3.1	6	391	1421	1	TIM_DROME	P49021 drosophila
318	1	776	3.1	6	392	1430	1	PTP_U_HUMAN	Q92729 homo sapien
319	1	776	3.1	6	393	1458	1	CUT4_SCHPO	Q9URV2 schizosacch
320	1	778	3.1	6	394	1529	1	SILT2_HUMAN	Q94813 homo sapien
321	1	786	3.1	6	395	1583	1	MIS4_SCHPO	Q09725 schizosacch
322	1	786	3.1	6	396	1584	1	BAIL_HUMAN	O14514 homo sapien
323	1	792	3.1	6	397	1591	1	TIAM_HUMAN	Q13009 homo sapien
324	1	794	3.1	6	398	1615	1	RIM1_RAT	Q9JIR4 rattus norv
325	1	797	3.1	6	399	1692	1	RIM1_HUMAN	Q86UR5 homo sapien

399	1	1744	CO4_HUMAN	P01028	homo sapien	472	1	Y9K_BPP4	P12552	bacterioph
400	1	1938	MYHD_HUMAN	Q9UKX3	homo sapien	473	1	Y27A_AERPE	P58322	aeropyrum p
401	1	1997	OTOF_HUMAN	Q9HCL0	homo sapien	474	1	RR15_MAIZE	P17703	zea mays (m
402	1	2210	RRPO_TACV	P20430	tacaribe vi	475	1	RR15_ORYSA	P12150	oryza sativ
403	1	2492	ATRX_HUMAN	P46100	homo sapien	476	1	RR15_WHEAT	P20283	triticum ae
404	1	2492	ATRX_PANTR	Q7YQM4	pan troglod	477	1	YORK_TTV1	P20283	triticum ae
405	1	2492	ATRX_PONPY	Q7YQM3	pongo pygma	478	1	DBH_STRDO	Q9XB22	thermoproc
406	1	2499	MPRI_BOVIN	P08169	bos taurus	479	1	VI79_FOWPV	Q9J554	fowlpox vir
407	1	3060	BPBE_HUMAN	Q8WXK8	homo sapien	480	1	CH10_STRGN	Q8VT59	streptococc
408	1	3214	BPAL_HUMAN	Q03001	homo sapien	481	1	FTSB_VIBPA	Q87LQ1	vibriopara
409	1	3386	POLG_DEN4	P09866	d genome po	482	1	FTSB_VIBSV	Q8DC61	vibriovuln
410	1	3386	PKHD_HUMAN	Q8TCZ9	homo sapien	483	1	SP3D_BACSU	P35281	bacillus su
411	1	4074	RYR2_HUMAN	Q92736	homo sapien	484	1	CH10_STRBO	Q8XJ15	streptococc
412	1	4567	RYR2_RABIT	P30957	oryctolagus	485	1	DBH_ANASP	P05514	anaeana sp
413	1	4569	RYR1_PIG	P16960	sus scrofa	486	1	DBH_XLFLA	Q8PE38	xylella fas
414	1	5037	RYR1_HUMAN	P11716	oryctolagus	487	1	DBH_XLFLT	Q8KJ13	vibriochol
415	1	5038	RYR1_HUMAN	P21817	homo sapien	488	1	FTSB_VIECH	P03476	influenza a
416	1	5065	EPPL_HUMAN	P58107	homo sapien	489	1	NRAM_IATKR	Q9T1T7	bacterioph
417	1	5171	BREA_HUMAN	Q94833	homo sapien	490	1	VAPD_HELPY	P11830	saccharopol
418	1	5348	EPPL_MOUSE	Q8X0W0	mus musculus	491	1	VLYS_BPAPS	P94797	francisella
419	1	5359	FMK7_PSEAE	Q53391	pseudomonas	492	1	ACP_SACER	P58251	clostridium
420	1	5361	PSBR_WHEAT	P12358	triticum ae	493	1	CH10_FRATU	P94797	francisella
421	1	5361	PETL_PORPU	P51221	porphyra pu	494	1	GAC1_CLOB	P18608	mus musculus
422	1	5361	PETM_CVAPA	P48366	cyanophora	495	1	HG14_MOUSE	P00089	rhodospiril
423	1	5361	E2F1_RAT	Q09139	rattus norv	496	1	CY22_RHOFU	Q24824	entamoeba h
424	1	5361	PPP5_RABIT	P55739	oryctolagus	497	1	PPPB_ENTHI	P03640	bacterioph
425	1	5361	CYC6_PROHO	P81244	prochloroth	498	1	VGE_BPG4	Q57621	methanococ
426	1	5361	ALL6_OLEBU	Q24172	olea europ	499	1	Y157_METJA	P03640	bacterioph
427	1	5361	LANA_STRPY	P36501	streptococc	500	1	Y398_MYCLE	Q33024	mycobacteri
428	1	5361	LANB_STRPY	Q54957	streptococc	501	1	CY22_RHOMO	P03088	rhodospiril
429	1	5361	FIXS_RHIME	P18399	rhizobium m	502	1	NUCG_SOYBN	P31174	glycine max
430	1	5361	RS21_UREPA	Q9PRL4	ureaplasma	503	1	VMT2_IABAN	P21430	influenza a
431	1	5361	SINI_BACIL	P22755	bacillus li	504	1	VMT2_IACKB	P36348	influenza a
432	1	5361	RS30_ORILA	Q9W6Y0	oryzias lat	505	1	VMT2_IACOW	P10921	influenza a
433	1	5361	RL29_SCHPO	Q92366	schizosacch	506	1	VMT2_IAPFR	P03492	influenza a
434	1	5361	RS14_LEPIN	Q9XD23	leptospira	507	1	VMT2_IATLE1	P26129	influenza a
435	1	5361	YLCE_ECOLI	P77087	escherichia	508	1	VMT2_IAMAN	P26130	influenza a
436	1	5361	YB53_METJA	Q58553	methanococ	509	1	VMT2_IASIN	P08382	influenza a
437	1	5361	YMA5_CABEL	P34521	caenorhabdi	510	1	VMT2_IATUD	P10920	influenza a
438	1	5361	COXA_MANSE	Q61494	manduca sex	511	1	VMT2_IATUD	P03490	influenza a
439	1	5361	SCX4_LEIQH	P83644	lelurus qui	512	1	VMT2_IATUD	P03490	influenza a
440	1	5361	CD52_CANFA	Q28896	canis faml	513	1	VMT2_IATUD	P03490	influenza a
441	1	5361	CERC_CERCA	Q17313	ceratitidis c	514	1	VMT2_IATUD	P03490	influenza a
442	1	5361	MT3_PIG	P55944	sus scrofa	515	1	VMT2_IATUD	P03490	influenza a
443	1	5361	YF75_METJA	Q58974	methanococ	516	1	VMT2_IATUD	P03490	influenza a
444	1	5361	FTSB_BUCAL	P57496	buchnera ap	517	1	VMT2_IATUD	P03490	influenza a
445	1	5361	YCX1_OENBE	P11673	oenothera b	518	1	VMT2_IATUD	P03490	influenza a
446	1	5361	VE7_BPVA	P08351	bovine papi	519	1	VMT2_IATUD	P03490	influenza a
447	1	5361	APEL_MOUSE	Q9R0R4	mus musculus	520	1	VMT2_IATUD	P03490	influenza a
448	1	5361	APEL_MOUSE	Q9R0R3	rattus norv	521	1	VMT2_IATUD	P03490	influenza a
449	1	5361	APEL_MOUSE	Q9R0R3	rattus norv	522	1	VMT2_IATUD	P03490	influenza a
450	1	5361	DERB_PHYBI	Q93221	agalychnis	523	1	VMT2_IATUD	P03490	influenza a
451	1	5361	DMS1_AGAN	Q93451	pachymedusa	524	1	VMT2_IATUD	P03490	influenza a
452	1	5361	DMS1_PACDA	Q8XWM9	ralstonia s	525	1	VMT2_IATUD	P03490	influenza a
453	1	5361	RL28_RALSO	Q8GR69	abirotrophia	526	1	VMT2_IATUD	P03490	influenza a
454	1	5361	DLTC_ABDIE	P56290	chlorella v	527	1	VMT2_IATUD	P03490	influenza a
455	1	5361	IF1C_CHUVU	Q980K7	sulfolobus	528	1	VMT2_IATUD	P03490	influenza a
456	1	5361	R17E_SULSO	Q34891	bacillus su	529	1	VMT2_IATUD	P03490	influenza a
457	1	5361	XJZB_BACSU	Q87RT8	vibriopara	530	1	VMT2_IATUD	P03490	influenza a
458	1	5361	EX7S_VIBPA	Q02958	ovis aries	531	1	VMT2_IATUD	P03490	influenza a
459	1	5361	KRHA_SHEEP	Q84424	chlamydia t	532	1	VMT2_IATUD	P03490	influenza a
460	1	5361	RL27_CHLTR	P12991	vibriopara	533	1	VMT2_IATUD	P03490	influenza a
461	1	5361	ATPL_VIBPA	Q8NFU4	homo sapien	534	1	VMT2_IATUD	P03490	influenza a
462	1	5361	PDGS_HUMAN	Q28580	ovis aries	535	1	VMT2_IATUD	P03490	influenza a
463	1	5361	KR71_SHEEP	P38613	sulfolobus	536	1	VMT2_IATUD	P03490	influenza a
464	1	5361	RLX_SULAC	P38613	sulfolobus	537	1	VMT2_IATUD	P03490	influenza a
465	1	5361	YSH7_CABEL	P50438	caenorhabdi	538	1	VMT2_IATUD	P03490	influenza a
466	1	5361	RBS2_ACECL	P16130	acetabulari	539	1	VMT2_IATUD	P03490	influenza a
467	1	5361	VGC_EPPHX	P03635	bacterioph	540	1	VMT2_IATUD	P03490	influenza a
468	1	5361	Y926_HAEIN	P44076	haemophilus	541	1	VMT2_IATUD	P03490	influenza a
469	1	5361	YB86_CLOB	Q97J00	clostridium	542	1	VMT2_IATUD	P03490	influenza a
470	1	5361	KR71_HUMAN	Q8IUC3	homo sapien	543	1	VMT2_IATUD	P03490	influenza a
471	1	5361	Y4EA_RHISN	P55424	rhizobium s	544	1	VMT2_IATUD	P03490	influenza a

545	5	2.6	107	1	KV6F_MOUSE	P04940	mus musculus	618	124	1	RL7_RHOSH	P02397	rhodobacter
546	5	2.6	107	1	KV6G_MOUSE	P04941	mus musculus	619	125	1	LR14_SULSO	O93774	sulfolobus
547	5	2.6	107	1	KV6J_MOUSE	P04943	mus musculus	620	126	1	ACTR_PAFHA	Q28928	papio hamad
548	5	2.6	107	1	KV6J_MOUSE	P04944	mus musculus	621	126	1	PFDA_AVEFA	Q9m4c4	avena fatua
549	5	2.6	107	1	SH3M_HUMAN	Q04jcs	homo sapien	622	126	1	RBS1_ACECL	P16129	acetabulari
550	5	2.6	107	1	SH3M_MOUSE	Q8bg73	mus musculus	623	126	1	RL7_BESVM	P02393	desulfovibri
551	5	2.6	107	1	YEL2_SCHPO	O13868	schizosacch	624	126	1	Y502_RICPR	Q9zd45	rickettsia
552	5	2.6	108	1	INS_PIG	P01315	sus scrofa	625	126	1	Y664_CHLMU	Q9PK09	chlamydia m
553	5	2.6	109	1	PRVA_RANES	P02627	rana escul	626	126	1	YP7_AGRU	P03867	agrobacteri
554	5	2.6	109	1	RL3E_METKA	O8xj0	methanopyru	627	127	1	CRCB_LEPIN	Q8ezs4	leptospira
555	5	2.6	109	1	RLA1_SCHPO	P17476	schizosacch	628	127	1	CRCB_PSEAE	Q9hw19	pseudomonas
556	5	2.6	109	1	RLA5_SCHPO	Q9uu78	schizosacch	629	127	1	FALP_MOUSE	Q9d159	mus musculus
557	5	2.6	109	1	VE7_HPV39	P24837	human papil	630	127	1	UCR7_KLULA	P49345	kluyveromyc
558	5	2.6	110	1	RPZ2_YEAST	Q04307	saccharomyc	631	127	1	Y491_PASMU	Q9cnel	pasteurella
559	5	2.6	111	1	KV12_RABIT	P01693	oryctolagus	632	127	1	YHHH_ECOLI	P28911	escherichia
560	5	2.6	111	1	PT00_YEAST	P38958	saccharomyc	633	127	1	YL35_ARCFU	O28145	archaeoglob
561	5	2.6	111	1	OR15_YEAST	P32344	saccharomyc	634	128	1	RL7_STRAT	P29342	streptomyce
562	5	2.6	111	1	RA2A_MAIZE	P46252	zea mays (m	635	128	1	YS98_MYCTU	O10819	mycobacteri
563	5	2.6	111	1	RL12_AERPE	Q9V9w9	aeropyrum p	636	128	1	YKND_BACSU	P45871	bacillus su
564	5	2.6	111	1	SDX_THEAC	O84390	chlamydia t	637	129	1	YKND_HUMAN	Q9np84	homo sapien
565	5	2.6	111	1	YH1T_CHLTR	P07188	drosofila	638	129	1	VDBP_CAMVC	P03552	cauliflower
566	5	2.6	112	1	CLP3_DROME	P07189	drosofila	639	129	1	VDBP_CAMVE	Q02967	cauliflower
567	5	2.6	112	1	VNFG_AZOCH	P15333	azotobacter	640	129	1	YKND_CAMVS	P03551	cauliflower
568	5	2.6	112	1	YH1T_BUCBP	P03289	human adeno	641	129	1	YKND_CAMVS	P52096	escherichia
569	5	2.6	112	1	YH1T_BUCBP	O89ag5	buchnera ap	642	129	1	DHSC_PARDE	Q59659	paracoccus
570	5	2.6	112	1	YH1T_BUCBP	O24415	zea mays (m	643	130	1	IN12_HUMAN	P09912	homo sapien
571	5	2.6	113	1	RA2B_MAIZE	O24415	zea mays (m	644	130	1	IN12_HUMAN	Q28808	pan troglod
572	5	2.6	113	1	YC71_MYCTU	Q11048	mycobacteri	645	130	1	LY6E_MOUSE	Q64253	mus musculus
573	5	2.6	114	1	RK20_CHLVU	P56352	chlorella v	646	130	1	YQJF_ECOLI	P42619	escherichia
574	5	2.6	114	1	TYBF_MOUSE	O54885	mus musculus	647	131	1	C79A_LOCFI	P45586	locusta mig
575	5	2.6	114	1	VG37_BPML5	Q05247	mycobacteri	648	131	1	C79A_LOCFI	P45587	locusta mig
576	5	2.6	114	1	YH1T_BUCAI	P57438	buchnera ap	649	131	1	Y293_AQUAE	O66843	aquifex aeo
577	5	2.6	114	1	YH1T_BUCAI	O67784	aquifex aeo	650	131	1	Y293_AQUAE	Q867x3	culex pipie
578	5	2.6	115	1	HYPA_AQUAE	O67133	aquifex aeo	651	132	1	ACES_CULPP	Q867x2	culex quing
579	5	2.6	115	1	PT21_STYPL	P28213	styela plic	652	132	1	ACES_CULPP	Q869c9	culex torre
580	5	2.6	115	1	RA2A_ARATH	Q981f7	arabidopsis	653	132	1	ACES_CULPP	P48935	cyamidium c
581	5	2.6	115	1	RA2B_ARATH	P51407	arabidopsis	654	132	1	ACES_CULPP	P08825	bombyx mori
582	5	2.6	115	1	TVC2_MOUSE	P03978	mus musculus	655	132	1	CHAZ_BOMMO	Q06455	xenopus lae
583	5	2.6	116	1	COAD_BPIKE	P03674	bacterioph	656	132	1	CRGS_XENLA	Q09190	schizosacch
584	5	2.6	116	1	MSCL_STAEP	O8cpca	staphylococ	657	133	1	CDD_SCHPO	Q939r0	fibrobacter
585	5	2.6	116	1	RBFA_CLOPE	Q8xj9	clostridium	658	133	1	YKRG_FIBSU	P16633	gracilaria
586	5	2.6	116	1	XKDD_BACSU	P39783	bacillus su	659	135	1	RS16_GRATE	P16633	gracilaria
587	5	2.6	116	1	YKDD_YEAST	P53222	saccharomyc	660	135	1	RS19_PIG	Q29308	sus scrofa
588	5	2.6	117	1	LV0A_HUMAN	P04211	homo sapien	661	135	1	TVC4_MOUSE	P06325	mus musculus
589	5	2.6	117	1	SP42_MOUSE	Q16550	homo sapien	662	136	1	CTD9_MOUSE	Q98q72	mycoplasma
590	5	2.6	117	1	Y051_RICCN	Q92199	mus musculus	663	136	1	RS9_MYCFU	P25352	saccharomyc
591	5	2.6	117	1	Y051_RICCN	Q92j16	rickettsia	664	136	1	YCR5_YEAST	Q9bvt0	homo sapien
592	5	2.6	118	1	Y13K_HCMVA	P03236	human cytom	665	137	1	CTD9_HUMAN	O27958	archaeoglob
593	5	2.6	118	1	Y687_THEMA	Q9wz13	thermotoga	666	137	1	IF2B_ARCFU	P56688	libinia ema
594	5	2.6	118	1	MCD1_HUMAN	P59942	homo sapien	667	137	1	MOIH_LIBEM	P21472	bacillus su
595	5	2.6	119	1	PA21_OXYSC	P00614	oxyuranus s	668	137	1	RS12_BACSU	P40761	bacillus su
596	5	2.6	119	1	RL24_METVA	P14034	methanococc	669	137	1	YUXX_BACSU	Q9ux90	sulfolobus
597	5	2.6	119	1	RS13_NITEU	P59755	nitrosomona	670	138	1	RL32_SULSO	P25097	simulium ir
598	5	2.6	119	1	SSB1_ANASP	Q820k3	anabaena sp	671	138	1	YMSF_IRV22	P51307	porphyra pu
599	5	2.6	120	1	DAN3_YEAST	P38155	saccharomyc	672	139	1	RK16_PORPU	O83766	treponema p
600	5	2.6	120	1	GALP_PIG	Q9tt95	sus scrofa	673	139	1	Y787_TREPA	P83179	brevicoryne
601	5	2.6	120	1	NU3C_ANTFO	Q31792	anthoceros	674	140	1	MYRO_BREBR	Q09389	caenorhabdi
602	5	2.6	120	1	PAUL_YEAST	P38924	saccharomyc	675	141	1	AT93_MOUSE	P56384	mus musculus
603	5	2.6	120	1	FAU2_YEAST	P32612	saccharomyc	676	141	1	FUR_BRUAE	O30976	bruceella ab
604	5	2.6	120	1	PAU6_YEAST	P52921	saccharomyc	677	141	1	FUR_BRUAE	O8yit8	bruceella me
605	5	2.6	120	1	YK65_YEAST	P53343	saccharomyc	678	141	1	FUR_BRUAE	Q8fz45	bruceella su
606	5	2.6	120	1	YK65_YEAST	P53055	saccharomyc	679	141	1	FUR_BRUAE	Q06549	saccharomyc
607	5	2.6	120	1	YHE6_YEAST	P38725	saccharomyc	680	142	1	CST8_MOUSE	P32766	mus musculus
608	5	2.6	121	1	CRNF_LYMST	P91758	lymaea sta	681	142	1	CST8_MOUSE	Q7v418	prochloroco
609	5	2.6	121	1	RS6_RICCN	Q92jk3	rickettsia	682	142	1	YQX1_CAEL	Q09557	caenorhabdi
610	5	2.6	121	1	ACFM_ARATH	P53665	arabidopsis	683	142	1	YQX1_CAEL	P40626	tetrahymena
611	5	2.6	122	1	CH10_AQUAE	O67942	aquifex aeo	684	143	1	HMBG_TETH	O26885	methanobact
612	5	2.6	122	1	CH5_PENNO	O97387	penaeus mon	685	143	1	Y771_METH	P80481	reclinomona
613	5	2.6	122	1	SLH1_HUMAN	O81zq5	homo sapien	686	144	1	C560_RECAM	P39019	homo sapien
614	5	2.6	122	1	YBEC_ECOLI	P33668	escherichia	687	144	1	RS19_HUMAN	P17074	rattus norv
615	5	2.6	122	1	YFC5_SHEPR	Q02482	shewanella	688	144	1	RS19_HUMAN	P38354	saccharomyc
616	5	2.6	123	1	LSM6_YEAST	Q06406	saccharomyc	689	144	1	YB8A_YEAST	O54266	streptococc
617	5	2.6	123	1	RR13_CYAME	P59758	cyandidiosch	690	145	1	SODM_STRPO		

691	1	SSIK_STRPT	145	2.6	5	O31702 streptomyce	764	158	1	NUGC_SPIOL	Q9m3ml spinacia ol
692	1	YTKA_BACSU	145	2.6	5	P40768 bacillus su	765	158	1	NUGC_TOBAB	P12201 nicotiana t
693	1	HBBI_MOUSE	146	2.6	5	P20088 mus musculu	766	159	1	ATPF_CLOAB	O05098 clostridium
694	1	HBBI_RAT	146	2.6	5	P02091 rattus norv	767	159	1	IF5A_DROME	Q9u6f8 drosophila
695	1	HBBI_MOUSE	146	2.6	5	P02089 mus musculu	768	159	1	NUGC_MAIZE	P19124 zea mays (m)
696	1	HBBI_MELE	146	2.6	5	P02055 meles meles	769	159	1	NUGC_ORYZA	P12200 oryza sativ
697	1	YIAC_ECOLI	146	2.6	5	P37664 escherichia	770	159	1	NUGC_WHEAT	Q95h60 triticum ae
698	1	CRCB_STAAM	147	2.6	5	Q99t86 staphylococ	771	159	1	RL22_THEMA	P38511 thermotoga
699	1	CRCB_STAAM	147	2.6	5	Q8nw04 staphylococ	772	159	1	SMG_VIBPA	P07kd8 vibrio para
700	1	IL4_MESAU	147	2.6	5	Q60440 mesocricetu	773	159	1	VGLI_VZVD	Q93k08 varicella-z
701	1	MSRE_CLOPE	147	2.6	5	Q8xj26 clostridium	774	159	1	Y165_CLOTE	Q899k8 clostridium
702	1	RS12_METUA	147	2.6	5	P14040 methanococc	775	159	1	Y000_CLOPE	Q8xh85 clostridium
703	1	RL16_CABEL	147	2.6	5	Q10129 caenorhabdi	776	160	1	CCMH_BRAJA	P45405 bradyrhizob
704	1	UCRH_YEAST	147	2.6	5	P22563 saccharomyc	777	160	1	HS21_HELAN	P46516 helianthus
705	1	FKBX_ECOLI	148	2.6	5	P14397 galleorhinus	778	160	1	U195_MOUSE	P12777 paracentrot
706	1	MYG_GALGA	148	2.6	5	P02206 heterodontu	779	160	1	NU6M_PARLI	P12777 paracentrot
707	1	ARGE_BACLI	148	2.6	5	O86130 bacillus li	780	160	1	U195_MOUSE	P12777 paracentrot
708	1	PERI_PPA	149	2.6	5	P09931 pisum sativ	781	160	1	U195_MOUSE	P12777 paracentrot
709	1	FLBI_CAUCR	149	2.6	5	P33977 caulobacter	782	161	1	ID4_HUMAN	P12777 paracentrot
710	1	PPDD_HABIN	149	2.6	5	P46233 haemophilus	783	161	1	ID4_HUMAN	P12777 paracentrot
711	1	Y919_METJA	149	2.6	5	Q58329 methanococc	784	161	1	RRAI_VIBCH	P12777 paracentrot
712	1	YK05_AQUAE	149	2.6	5	Q67808 aquifex aeo	785	161	1	VANZ_ENTFC	P12777 paracentrot
713	1	ALL5_HVBVR	150	2.6	5	Q39967 hevea bras	786	161	1	CRTZ_ALCSP	P12777 paracentrot
714	1	GRDA_CLOPU	150	2.6	5	P26970 clostridium	787	162	1	RI18_ADEP1	P12777 paracentrot
715	1	NRDI_MCTCU	150	2.6	5	P95107 mycobacteri	788	162	1	PHCA_SYNTP6	P12777 paracentrot
716	1	RLI5_RICPR	150	2.6	5	Q9ZC84 rickettsia	789	162	1	YAB4_STROO	P12777 paracentrot
717	1	RS13_HUMAN	150	2.6	5	Q02546 homo sapien	790	162	1	E1B5_ADEL2	P12777 paracentrot
718	1	RS13 ICTPU	150	2.6	5	P47772 ictalurus p	791	163	1	PI11_HUMAN	P12777 paracentrot
719	1	RS13_XENLA	150	2.6	5	P49393 xenopus lae	792	163	1	SAK_STAAM	P12777 paracentrot
720	1	RS13_YEAST	150	2.6	5	P05756 saccharomyc	793	163	1	Y057_NPVOP	P12777 paracentrot
721	1	SSB_THETHN	150	2.6	5	Q8r6m2 thermoanaer	794	163	1	Y1YK_BACSU	P12777 paracentrot
722	1	SSRP_BACTN	150	2.6	5	Q8abd1 bacteroides	795	163	1	ID1_RAT	P12777 paracentrot
723	1	YF59_MYCLE	150	2.6	5	Q925j2 mycobacteri	796	164	1	MAFF_HUMAN	P12777 paracentrot
724	1	CRPE_CHLTR	151	2.6	5	P26757 chlamydia t	797	164	1	MCRD_HUMAN	P12777 paracentrot
725	1	SP17_HUMAN	151	2.6	5	Q15506 homo sapien	798	164	1	NUOE_ECOLI	P12777 paracentrot
726	1	SP17_MACFA	151	2.6	5	Q19021 macaca fasc	799	164	1	NUOE_ECOLI	P12777 paracentrot
727	1	TERS_BPSF6	151	2.6	5	Q25153 drosophila	800	164	1	NUOE_ECOLI	P12777 paracentrot
728	1	UCB6_DROME	151	2.6	5	Q45584 bacillus su	801	165	1	NGK7_HUMAN	P12777 paracentrot
729	1	YBKK_BACSU	151	2.6	5	P19242 pisum sativ	802	165	1	RS13_SULSO	P12777 paracentrot
730	1	YXAI_BACSU	151	2.6	5	Q42108 bacillus su	803	165	1	YF62_STRAP	P12777 paracentrot
731	1	HS21_PEA	152	2.6	5	Q99t10 staphylococ	804	165	1	Y473_STRPY	P12777 paracentrot
732	1	PHEB_STAAM	152	2.6	5	P19242 pisum sativ	805	165	1	YF62_STRAP	P12777 paracentrot
733	1	RS13_PYPAE	152	2.6	5	Q82tv0 probaculum	806	165	1	NUOE_ECOLI	P12777 paracentrot
734	1	YD58_METUA	152	2.6	5	Q58753 methanococc	807	166	1	NUOE_ECOLI	P12777 paracentrot
735	1	YF63_METUA	152	2.6	5	Q58958 methanococc	808	166	1	NUOE_ECOLI	P12777 paracentrot
736	1	YF63_METUA	152	2.6	5	Q31554 bacillus su	809	166	1	NUOE_ECOLI	P12777 paracentrot
737	1	YF63_METUA	152	2.6	5	Q31554 bacillus su	810	167	1	CHCC_ANTPO	P12777 paracentrot
738	1	YF63_METUA	152	2.6	5	Q67706 aquifex aeo	811	167	1	CHCC_ANTPO	P12777 paracentrot
739	1	MLR_PATSP	153	2.6	5	P02613 patinopecte	812	167	1	YB20_AQUAE	P12777 paracentrot
740	1	SODC_YEAST	153	2.6	5	P00445 saccharomyc	813	167	1	YF57_ARCFU	P12777 paracentrot
741	1	PFDA_AERPE	154	2.6	5	Q9ydv28 aeropyrum p	814	168	1	ID1_MOUSE	P12777 paracentrot
742	1	PFDA_HALNI	154	2.6	5	Q9ydv28 aeropyrum p	815	168	1	ILVH_METTH	P12777 paracentrot
743	1	YM13_MARPO	154	2.6	5	P38457 marchantia	816	168	1	RIAB_CVCAI	P12777 paracentrot
744	1	2SS2_CARPA	154	2.6	5	P30233 capparis ma	817	169	1	AROK_COREF	P12777 paracentrot
745	1	COX4_YEAST	155	2.6	5	P04037 saccharomyc	818	169	1	AROK_COREF	P12777 paracentrot
746	1	ID1_HUMAN	155	2.6	5	P41134 homo sapien	819	169	1	C560_BOVIN	P12777 paracentrot
747	1	KE4_PIG	155	2.6	5	Q29175 sus scrofa	820	169	1	CRG2_RANTE	P12777 paracentrot
748	1	MGSA_THEMA	155	2.6	5	Q9x0r7 thermotoga	821	169	1	CRG2_RANTE	P12777 paracentrot
749	1	RS7_UREPA	155	2.6	5	Q55827 ureaplasma	822	169	1	CRG2_RANTE	P12777 paracentrot
750	1	Y481_SYNY3	155	2.6	5	Q55827 ureaplasma	823	169	1	CRG2_RANTE	P12777 paracentrot
751	1	Y481_SYNY3	155	2.6	5	Q55827 ureaplasma	824	170	1	CRG2_RANTE	P12777 paracentrot
752	1	MLR_AEQIR	156	2.6	5	P13543 aequipecten	825	170	1	CRG2_RANTE	P12777 paracentrot
753	1	MOAC_METKA	156	2.6	5	Q8txv5 methanopyru	826	170	1	CRG2_RANTE	P12777 paracentrot
754	1	PYRI_METKA	156	2.6	5	Q8tvb1 methanopyru	827	171	1	CRG2_RANTE	P12777 paracentrot
755	1	RS7_CARRU	156	2.6	5	Q8aig8 carsonella	828	171	1	CRG2_RANTE	P12777 paracentrot
756	1	CREA_ECOLI	157	2.6	5	P08367 escherichia	829	171	1	CRG2_RANTE	P12777 paracentrot
757	1	ISPF_CHLTF	157	2.6	5	Q8kc25 chlorobium	830	171	1	CRG2_RANTE	P12777 paracentrot
758	1	Y406_MYCPN	157	2.6	5	Q50325 mycoplasma	831	172	1	CRG2_RANTE	P12777 paracentrot
759	1	CT13_MOUSE	158	2.6	5	Q9cird4 mus musculu	832	172	1	CRG2_RANTE	P12777 paracentrot
760	1	NUGC_ARATH	158	2.6	5	P56754 arabidopsis	833	172	1	CRG2_RANTE	P12777 paracentrot
761	1	NUGC_LOTJA	158	2.6	5	Q9bbt6 lotus japon	834	172	1	CRG2_RANTE	P12777 paracentrot
762	1	NUGC_LOTJA	158	2.6	5	Q9bbt6 lotus japon	835	172	1	CRG2_RANTE	P12777 paracentrot
763	1	NUGC_OENHO	158	2.6	5	Q92309 lupinus lut	836	172	1	CRG2_RANTE	P12777 paracentrot

837	1	173	5	2.6	1	110	910	185	1	Y754_METUA	Q58164 methanococc
838	1	173	5	2.6	1	911	911	185	1	YCF4_BRAOL	Q31910 brassica ol
839	1	173	5	2.6	1	912	912	186	1	AROK_BACSU	P37944 bacillus su
840	1	173	5	2.6	1	913	913	186	1	DMML_METFL	Q50425 methylobaci
841	1	173	5	2.6	1	914	914	186	1	Y783_METJA	Q58193 methanococc
842	1	173	5	2.6	1	915	915	186	1	YCF4_OENHO	Q9mt11 oenothera h
843	1	173	5	2.6	1	916	916	187	1	Y503_TREPA	Q83516 treponema p
844	1	173	5	2.6	1	917	917	187	1	YCF4_MESVI	Q9mun8 mesostigma
845	1	173	5	2.6	1	918	918	188	1	GTS2_CAEEL	O16115 caenorhabdi
846	1	174	5	2.6	1	919	919	188	1	HSLV_CAUCR	Q9a239 caulobacter
847	1	174	5	2.6	1	920	920	188	1	YCF4_GLOVI	Q7uph6 gloebacter
848	1	175	5	2.6	1	921	921	189	1	KTHI_SULSO	Q93341 caenorhabdi
849	1	175	5	2.6	1	922	922	189	1	LVNI_LYTVA	P15262 lytechinus
850	1	175	5	2.6	1	923	923	189	1	PSBY_ARATH	Q49347 arabidopsis
851	1	175	5	2.6	1	924	924	189	1	RS9_CAEEL	Q20228 caenorhabdi
852	1	175	5	2.6	1	925	925	189	1	3MGH_DEIRA	Q9rsq0 deinococcus
853	1	176	5	2.6	1	926	926	190	1	APOM_RAT	P14630 rattus norv
854	1	176	5	2.6	1	927	927	190	1	HDED_ECOLI	P26603 escherichia
855	1	176	5	2.6	1	928	928	190	1	RT23_HUMAN	Q9y3d9 homo sapien
856	1	176	5	2.6	1	929	929	190	1	VIS1_HUMAN	P28677 homo sapien
857	1	176	5	2.6	1	930	930	190	1	VIS2_RAT	P35332 rattus norv
858	1	176	5	2.6	1	931	931	191	1	PGHD_SHEEP	Q9xsm0 ovis aries
859	1	176	5	2.6	1	932	932	191	1	YL27_STRCO	P40182 streptomyc
860	1	177	5	2.6	1	933	933	192	1	MOBA_NEIMA	Q9jua5 neisseria m
861	1	177	5	2.6	1	934	934	192	1	MOBA_NEIMA	P58747 neisseria m
862	1	177	5	2.6	1	935	935	192	1	Y857_METTH	O26945 methanobact
863	1	177	5	2.6	1	936	936	192	1	YC08_YEAST	P37261 saccharomyc
864	1	178	5	2.6	1	937	937	193	1	CERR_MOUSE	P23435 homo sapien
865	1	178	5	2.6	1	938	938	193	1	CLPI_CYPAP	Q9r171 mus musculu
866	1	178	5	2.6	1	939	939	194	1	FLR_DESGI	Q36863 cyanophora
867	1	178	5	2.6	1	940	940	194	1	KADI_MOUSE	Q9k1t1 desulfovibr
868	1	178	5	2.6	1	941	941	194	1	KADI_MOUSE	Q9roy5 mus musculu
869	1	179	5	2.6	1	942	942	194	1	KADI_MOUSE	P39069 rattus norv
870	1	179	5	2.6	1	943	943	194	1	KADI_MOUSE	P29999 african swi
871	1	179	5	2.6	1	944	944	194	1	VP30_ASFE7	Q58069 methanococc
872	1	179	5	2.6	1	945	945	194	1	Y653_METJA	Q9rt91 deinococcus
873	1	179	5	2.6	1	946	946	194	1	YD16_HABIN	Q8p319 xanthomonas
874	1	180	5	2.6	1	947	947	195	1	PAAD_DEIRA	P18555 african swi
875	1	180	5	2.6	1	948	948	195	1	TATB_XANCP	P40958 saccharomyc
876	1	181	5	2.6	1	949	949	196	1	KITH_ASFB7	Q8v7b1 arabidopsis
877	1	181	5	2.6	1	950	950	196	1	MAD2_YEAST	P10940 escherichia
878	1	181	5	2.6	1	951	951	196	1	SOHI_ARATH	P34204 african swi
879	1	181	5	2.6	1	952	952	196	1	UHPA_ECOLI	Q8p7u5 xanthomonas
880	1	181	5	2.6	1	953	953	196	1	VP32_ASFB7	Q8p7u5 xanthomonas
881	1	181	5	2.6	1	954	954	196	1	YPI3_XANCP	Q8p7u5 xanthomonas
882	1	181	5	2.6	1	955	955	196	1	YQ89_XANCP	Q8p7u5 xanthomonas
883	1	181	5	2.6	1	956	956	197	1	CFI2_MEDSA	P28013 medicago sa
884	1	181	5	2.6	1	957	957	197	1	DEM1_PHYSA	P05422 phyllomedus
885	1	182	5	2.6	1	958	958	197	1	RECR_FUSNN	Q8rg96 fusobacteri
886	1	182	5	2.6	1	959	959	197	1	RL18_SULAC	O05640 sulfolobus
887	1	182	5	2.6	1	960	960	197	1	YCB7_SEDE	P29940 pseudomonas
888	1	182	5	2.6	1	961	961	197	1	YCB7_SEDE	P05421 phylomedus
889	1	182	5	2.6	1	962	962	198	1	DEM2_PHYSA	O61907 mus musculu
890	1	182	5	2.6	1	963	963	198	1	PEMT_MOUSE	Q08388 rattus norv
891	1	182	5	2.6	1	964	964	198	1	PEMT_MOUSE	Q00579 streptococc
892	1	182	5	2.6	1	965	965	198	1	RECU_STROR	P38074 streptococc
893	1	182	5	2.6	1	966	966	198	1	RECU_STROR	P56876 helicobacte
894	1	182	5	2.6	1	967	967	198	1	TSAA_HELPJ	P54603 bacillus su
895	1	182	5	2.6	1	968	968	198	1	YHCS_BACSU	Q8cs90 staphylococ
896	1	183	5	2.6	1	969	969	199	1	AROK_MYCLE	P76209 escherichia
897	1	183	5	2.6	1	970	970	199	1	TSAA_BUCBP	O40958 equine aden
898	1	183	5	2.6	1	971	971	200	1	ISPZ_BRAJA	Q9ntu7 homo sapien
899	1	183	5	2.6	1	972	972	200	1	NADD_SYNY3	P82664 homo sapien
900	1	183	5	2.6	1	973	973	200	1	PCXA_PSEPU	Q9b111 homo sapien
901	1	183	5	2.6	1	974	974	201	1	RUVA_STAEP	Q9p720 neuropsora
902	1	184	5	2.6	1	975	975	201	1	YDJM_ECOLI	P48230 homo sapien
903	1	184	5	2.6	1	976	976	201	1	ADEN_ADEB2	Q06241 enterococcu
904	1	184	5	2.6	1	977	977	201	1	CERL_HUMAN	
905	1	184	5	2.6	1	978	978	201	1	RT10_HUMAN	
906	1	184	5	2.6	1	979	979	202	1	CTD6_HUMAN	
907	1	185	5	2.6	1	980	980	202	1	RL16_NEUCR	
908	1	185	5	2.6	1	981	981	202	1	T454_HUMAN	
909	1	185	5	2.6	1	982	982	202	1	VANX_ENTFC	



983 2.6 202 1 YO15\_CABEL  
984 2.6 203 1 ARDH\_DICDI  
985 2.6 203 1 CLDM\_HUMAN  
986 2.6 203 1 HPR\_EACSV  
987 2.6 203 1 YNU3\_YEAST  
988 2.6 204 1 EVGA\_ECOLI  
989 2.6 204 1 GIDB\_COMBU  
990 2.6 204 1 KGUA\_BACHD  
991 2.6 204 1 LEF2\_NPVOF  
992 2.6 204 1 RRA2\_HUMAN  
993 2.6 204 1 R88\_GRIJA  
994 2.6 204 1 YKQ3\_SCHPO  
995 2.6 205 1 V001\_F0PVP  
996 2.6 206 1 GIDB\_BACTN  
997 2.6 206 1 GTS9\_CAESL  
998 2.6 206 1 PYRE\_ANASP  
999 2.6 206 1 RUVA\_MYCPN  
1000 2.6 206 1 VATE\_METUA

Q7Z142 caenorhabdi  
P36416 dictyosteli  
Q8N7P3 homo sapien  
P11065 bacillus su  
P40163 saccharomyc  
P30854 escherichia  
P94614 coxiella bu  
Q8K9Y2 bacillus ha  
Q65370 oryzaia peeu  
P17082 homo sapien  
Q9ZT56 griffithsia  
Q9P6M2 schizosacch  
Q9ICH6 fowlpox vir  
Q8A8M2 bacteroides  
Q21743 caenorhabdi  
Q8YM41 anabaena sp  
P75243 mycoplasma  
Q57673 methanococc

Q7Z142 dictyosteli  
P36416 dictyosteli  
Q8N7P3 homo sapien  
P11065 bacillus su  
P40163 saccharomyc  
P30854 escherichia  
P94614 coxiella bu  
Q8K9Y2 bacillus ha  
Q65370 oryzaia peeu  
P17082 homo sapien  
Q9ZT56 griffithsia  
Q9P6M2 schizosacch  
Q9ICH6 fowlpox vir  
Q8A8M2 bacteroides  
Q21743 caenorhabdi  
Q8YM41 anabaena sp  
P75243 mycoplasma  
Q57673 methanococc

FT METAL 89 89 CALCIUM (VIA CARBONYL OXYGEN)  
FT METAL 91 91 CALCIUM (VIA CARBONYL OXYGEN)  
FT METAL 93 93 CALCIUM (VIA CARBONYL OXYGEN)  
FT METAL 116 116 CALCIUM (BY SIMILARITY)  
FT CONFLICT 157 157 MISSING (IN REF. 1)  
SQ SEQUENCE 195 AA; 21659 MW; C00C817F81D68A70 CRC64;

Query Match 70.6%; Score 137; DB 1; Length 195;  
Best Local Similarity 100.0%; Pred. No. 6.1e-134;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGLFVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSPFESVNSYFDSFLELLGGK 60  
DB 1 MKLASGLFVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSPFESVNSYFDSFLELLGGK 60  
QY 61 NGVCQYRCRYGKAMPKPRGYKQEPNGCGSYFLGLKVPESMDLGIKAMTKCCNOLDVCYD 120  
DB 61 NGVCQYRCRYGKAMPKPRGYKQEPNGCGSYFLGLKVPESMDLGIKAMTKCCNOLDVCYD 120  
QY 121 TCGANKYRCDAKFRWCL 137  
DB 121 TCGANKYRCDAKFRWCL 137

RESULT 2  
PA2Z\_MOUSE  
ID PA2Z\_MOUSE STANDARD; PRT; 195 AA.  
AC Q99E27;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Group XIII secretory phospholipase A2-like protein precursor (GXIII  
DE SPLA2-like)  
DE PLA2G13 OR FKS71.  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 x DBA;  
RA Wang Y.-G., Gong L.;  
RT "Cloning and characterization of FKS71, a novel gene encoding group  
XIII secreted phospholipase A2";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Not known; does not seem to have catalytic activity.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF339738; AA01739.1; --  
CC MGD; MGI:1917086; Pla2g13.  
CC InterPro; IPR000886; ER\_target\_S.  
CC InterPro; IPR001211; PhospholipaseA2.  
CC PROSITE; PS00119; PA2\_ASP; FALSE NEG.  
CC PROSITE; PS00118; PA2\_HIS; FALSE NEG.  
CC PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
CC SIGNAL 1 19 POTENTIAL.  
CC CHAIN 20 195 GROUP XIII SECRETORY PHOSPHOLIPASE A2-  
CC METAL 89 89 CALCIUM (VIA CARBONYL OXYGEN)



	91	91	(BY SIMILARITY)
METAL			CALCIUM (VIA CARBONYL OXYGEN)
T			(BY SIMILARITY).
T			CALCIUM (VIA CARBONYL OXYGEN)
T			(BY SIMILARITY).
T			CALCIUM (BY SIMILARITY).
T			86F8B653BD08DA24 CRC64.
T			116
METAL			116
SEQUENCE			195 BA. 21736 MW.

Query Match	19.6%;	Score 38;	DB 1; Length 195;
Best Local Similarity	100.0%;	Pred. No. 1.3e-31;	
Conservative	0.	Mismatches 0;	Indels 0; Gaps 0;

100 SMDLGIPAMTKCCNQILDVCDTCGANKYRCDAKFQWCL 137  
100 SMDLGIPAMTKCCNQILDVCDTCGANKYRCDAKFQWCL 137  
100 SMDLGIPAMTKCCNQILDVCDTCGANKYRCDAKFQWCL 137

RESULT 3	ADEN_ADE41	STANDARD;	PRT;	214 AA.
ID	ADEN_ADE41			
AC	P11836;			
DT	01-OCT-1989 (Rel. 12, Created)			
OT	01-OCT-1989 (Rel. 12, last sequence update)			
UP	16-OCT-2001 (Rel. 40, last annotation update)			
DE	Adenain (EC 3.4.22.39) (Endoprotease) (late L3 23 kDa protein) .			
OS	Human adenovirus type 41.			
DS	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.			
OC	NCBI TaxID=10524;			
OX				

PP SEQUENCE FROM N.A.  
 RX MEDLINE=88160034; PubMed=3279700;  
 RA Vos H.I., der Lee F.M., Reemst A.M.C.B., van Loon A.E.,  
 RA Sussenbach J.S.;  
 RA "The genes encoding the DNA binding protein and the 23K protease of  
 RA adenovirus types 40 and 41.";  
 RT adenovirus types 40 and 41.";  
 RT Virology 163:1-10(1988).  
 RN [2]  
 RN SEQUENCE OF 1-198 FROM N.A.

STRAIN=RAK; RC  
TOOGOOD C.I.A., Murali R., Burnett M., Hay R.T.;  
Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: THIOLEPTASE CLEAVING SPECIFIC GLY-ALA PEPTIDES IN A  
NUMBER OF VIRAL PRECURSOR PROTEINS (TERMINAL, IIA, VI, VII, VIII,  
IIA AND MU) WHICH ARE REQUIRED FOR VIRION MATURATION. ALSO CLEAVES  
HOST CELLS CYTOSKELETAL KERATINS K7 AND K18.  
-!- CATALYTIC ACTIVITY: Cleaves proteins of the adenovirus and its  
host cell at two consensus sites: -Yaa-Xaa-Gly-Gly-I-Xaa- and  
-Yaa-Xaa-Gly-Xaa-I-Gly- (in which Yaa is Met, Ile or Leu, and Xaa  
is any amino acid).  
-!- SIMILARITY: Belongs to peptidase family C5.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation  
at the European Bioinformatics Institute. There are no restrictions on  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement. See <http://www.isb-sib.ch/announcement>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
-----

ENBL; M21163; AAA42462.1; -			
DR			
ENBL; X51783; CAA36080.1; -			
DR			
PIR; E28645; W2AD41.			
DR			
HSP; P03252; 1A VP.			
DR			
MEROPS; C05.001; -			
DR			
InterPro; IPR000835; peptidase C5.			
DR			
Pfam; PF00770; Peptidase C5; 1-			
DR			
PRINTS; PR00703; ADVENTOFASE.			
DR			
ProDom; PD003705; Peptidase C5; 1.			
DR			
Hydrolase; Thiol protease; late protein; autocatalytic cleavage			
KW			
FT	46	47	CLEAVAGE (AUTO-) (POTENTIAL).
FT	SITE		
FT	ACT SITE	54	54
FT	ACT_SITE	71	71
FT	ACT_SITE	122	122
FT			BY SIMILARITY.
FT			BY SIMILARITY.
FT			BY SIMILARITY.

SQ SEQUENCE 214 AA; 24482 MW; 66602CBG786D2371 CRC64;  
4.1%; Score 8; DB 1; Length 214;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 GCGSYFLG 94  
16 GCGSYFLG 23  
Db

RESULT 4	STANDARD;	PRT;
RLA2 YEAST	ID_RLA2 YEAST	106 AA.

01-NOV-1988 (Rel. 09, Created)  
01-NOV-1988 (Rel. 09, Last sequence update)  
11-NOV-1988 (Rel. 09, Last annotation update)  
16-OCT-2001 (Rel. 40, Last annotation update)  
60S acidic ribosomal protein L2-alpha (A2) (L44) (L12E1B).  
RPP2A OR RPLA2 OR L12E1B OR RPA2 OR RPL44 OR YOL039W.  
Saccharomyces cerevisiae (Baker's yeast).  
Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetes; Saccharomycetes.

OX	NCBI_IAXID=49552;
RN	[1]
RP	SEQUENCE FROM N.A.

RX MEDLINE=88233394; PubMed=3287329;  
RA Mitsui K., Tsurugi K.;  
RT "cDNA and deduced amino acid sequence of acidic ribosomal protein A2  
RT from *Saccharomyces cerevisiae*.";  
RL Nucleic Acids Res. 16:3575-3575(1988).

SEQUENCE FROM N.A.  
RX MEDLINE=88243786; PubMed=2837476;  
RA Remacha M., Saenz-Robles M.T., Vilella M.D., Ballesta J.P.G.;  
RT "Independent genes coding for three acidic proteins of the large  
RT ribosomal subunit from *Saccharomyces cerevisiae*.";  
RV J. Biol. Chem. 263:9094-9101(1988).

SEQUENCE FROM N.A.  
 RP STRAIN=SR26-12C;  
 RC MEDLINE=90130289; PubMed=2404943;  
 RX Newton C.H., Shaiman L.C., Yee J., Dennis P.P.;  
 RA "A family of genes encode the multiple forms of  
 RT cerevisiae ribosomal proteins equivalent to the  
 RL protein and a single form of the L10-equivalent  
 RL J. Bacteriol. 172:579-588(1990).  
 RL the Saccharomyces  
 RL the Escherichia coli L1  
 RL ribosomal protein."

RP SEQUENCE FROM N.A.  
RA Ansgore W., Benes V., Rechmann S., Schwager C., Teodoru C.,  
RA Voss H., Wiemann S.;  
RA 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2

[5] SEQUENCE FROM N.A.  
RN Habbig B., Hattenhorst U., Hollenberg C.P., Ramezani Rad M.;  
RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RL  
CC  
CC -!- FUNCTION: Plays an important role in the elongation step of  
CC protein synthesis

-1- PSMUNIL: F1 and F2 exist as dimers.  
CC  
-1- PTM: Phosphorylated [By similarity].  
CC  
-1- MISCCELLANEOUS: Yeasts contain 4 individual small ribosomal A  
CC  
proteins (RPA) which can be classified into two couples of simi  
CC  
but not identical sequences. Each couple is distinctly related  
CC  
one of the two A proteins present in multicellular organisms.  
CC  
-1- SWEDEN: The H12P family of ribosomal proteins.

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

```

C EMBL; X06958; CAA30028.1; -
C EMBL; J03760; AAA34971.1; -
R EMBL; M26503; AAA34735.1; -
R EMBL; M27481; CAA99041.1; -
R PIR; B28104; R5BYIB.
R GerMOnline; 143461; -
R SGD; S0005399; RPP2A.
R InterPro; IPR001813; Ribosomal_60S.
R Pfam; PF00428; 60S_ribosomal; 1.
R Ribosomal protein; Phosphorylation; Multigene family.
QW SEQUENCE 106 AA; 10746 MW; 2227AFPA35EIA32E CRC64;

Query Match 3.6%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
Db 84 ABEKEE 90

RESULT 5
RLA3_YEAST
ID_RLA3_YEAST STANDARD; PRT; 106 AA.
AC P10622;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60S acidic ribosomal protein P1-beta (L12E11B)
EN RPB1B OR RPLA3 OR L12E11B OR RPL44P OR YDL130W.
PE RPB1B OR RPLA3 OR L12E11B OR RPL44P OR YDL130W.
PR Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_TaxID=4932;
RN NCBI_TaxID=4932;
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Brueckner M., Schaefer M., Wagner G.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays an important role in the elongation step of
CC protein synthesis.
CC -!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
CC -!- MISCELLANEOUS: Yeasts contain 4 individual small ribosomal A
CC proteins (RPA) which can be classified into two couples of similar
CC but not identical sequences. Each couple is distinctly related to
CC one of the two A proteins present in multicellular organisms.
CC -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC SEQUENCE FROM N.A.
CC STRAIN=SR26-12C;
CC MEDLINE=90130289; PubMed=2404943;
CC Newton C.H., Shimmis L.C., Yee J., Dennis P.P.;
CC "A family of genes encode the multiple forms of the Saccharomyces
CC cerevisiae ribosomal proteins equivalent to the Escherichia coli L12
CC protein and a single form of the L10-equivalent ribosomal protein.";
CC J. Bacteriol. 172:579-588 (1990).
CC [3]
CC SEQUENCE FROM N.A.
CC Rieger M., Mueller-Auer S., Brueckner M., Schaefer M., Wagner G.;
CC Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays an important role in the elongation step of
CC protein synthesis.
CC -!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
CC -!- MISCELLANEOUS: Yeasts contain 4 individual small ribosomal A
CC proteins (RPA) which can be classified into two couples of similar
CC but not identical sequences. Each couple is distinctly related to
CC one of the two A proteins present in multicellular organisms.
CC -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC

```

```

DR EMBL; M19238; AAA34973.1; -
DR EMBL; M26507; AAA34734.1; -
DR EMBL; Z74178; CAA98698.1; -
DR PIR; C28104; R8BY2B.
DR GerMOnline; 140372; -
DR SGD; S0002288; RPF1B.
DR InterPro; IPR001813; Ribosomal_60S.
DR Pfam; PF00428; 60S_ribosomal; 1.
KW Ribosomal protein; Phosphorylation; Multigene family.
SQ SEQUENCE 106 AA; 10667 MW; EAED4F748653E0DC CRC64;

Query Match 3.6%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
Db 84 ABEKEE 90

RESULT 6
RLA1_CLAHE
ID_RLA1_CLAHE STANDARD; PRT; 110 AA.
AC P50344;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 60S acidic ribosomal protein P1 (Allergen Cla h 12) (Cla h XII).
EN CLAH12.
PE Cladosporium herbarum.
PR Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothromycetes incertae sedis;
OC Mycosphaerellaceae; Davidiella.
CX NCBI_TaxID=29918;
RN [1]
RP SEQUENCE FROM N.A.
RA Oberkolfer H.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays an important role in the elongation step of
CC protein synthesis.
CC -!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X85180; CAA59463.1; -
CC InterPro; IPR001813; Ribosomal_60S.
CC Pfam; PF00428; 60S_ribosomal; 1.
CC Ribosomal protein; Phosphorylation; Allergen.
SQ SEQUENCE 110 AA; 11020 MW; 1B201BC2553DAC42 CRC64;

Query Match 3.6%; Score 7; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
Db 93 ABEKEE 99

RESULT 7
RLA4_YEAST
ID_RLA4_YEAST STANDARD; PRT; 110 AA.
AC P02400;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)

```

```

SQ SEQUENCE 110 AA; 11050 MW; EC45406CB5F199F4 CRC64;

Query Match 3.6%; Score 7; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AEEKKE 193
    |||||
DB 88 AEEKKE 94

RESULT 8
RLA4 CLAEH
ID FLA4 CLAEH STANDARD; PRT; 111 AA.
AC P42039;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE 60S acidic ribosomal protein P2 (Minor allergen Cla h 4) (Cla h IV).
GN CLAH4
OS Cladosporium herbarum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis;
OC Mycosphaerellaceae; Davidiella.
NCBI_TaxID=29918;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=280202-Berlin;
RC MEDLINE=95206305; PubMed=7898496;
RX Achatz G., Oberkofler H., Lechenauer E., Simon B., Unger A.,
RA Kandler D., Eberhart C., Prillinger H., Kraft D., Breitenbach M.;
RT "Molecular cloning of major and minor allergens of Alternaria
RT alternata and Cladosporium herbarum.";
RL Mol. Immunol. 32:213-227(1995).
RN [2]
RP REVISIONS TO 13; 38-41 AND 93.
RL Simon-Nobbe B.;
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Plays an important role in the elongation step of
CC protein synthesis.
CC -I- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
CC -I- PTM: Phosphorylated (By similarity).
CC -I- ALLERGEN: Causes an allergic reaction in human.
CC -I- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC -I- CAUTION: Two distinct proteins have been termed allergen
CC Cla h 4.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; X78223; CAA55067.2; --
DR InterPro; IPR001813; Ribosomal 60S.
DR Pfam; PF00428; 60s_Ribosomal; 1.
KW Ribosomal protein; Phosphorylation; Multigene family; Allergen.
SQ SEQUENCE 111 AA; 11105 MW; C7B65C6AD997B76A CRC64;

Query Match 3.6%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AEEKKE 193
    |||||
DB 94 AEEKKE 100

RESULT 9
TD53 HUMAN STANDARD; PRT; 204 AA.
ID TD53 HUMAN STANDARD; PRT; 204 AA.

```

```

C 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
E Tumor protein D53 (hd53) (D52-like 1).
N TPDS2L1.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
C NCBI_TaxID=9606;
[1]
P TISSUE=Breast carcinoma;
C MEDLINE=97001154; PubMed=8812487;
X Byrne J.A., Mattei M.-G., Basset P.;
T "Definition of the tumor protein D52 (TPD52) gene family through
T cloning of D52 homologues in human (hd53) and mouse (md52).";
T Genomics 35:523-532(1996).
L
L SEQUENCE 204 AA; 22515 MW; 6B3C36D5C0653C9 CRC64;
FT DOMAIN 22 73 COILED COIL (POTENTIAL).
SQ SEQUENCE 204 AA; 22515 MW; 6B3C36D5C0653C9 CRC64;

INTERACTIONS.
BYRNE J.A., Nourae C.R., Basset P., Gunning P.;
"Identification of homo- and heteromeric interactions between members
of the breast carcinoma-associated D52 protein family using the yeast
two-hybrid system.";
Oncogene 16:873-881(1998).
RL NCBI_TaxID=10090;
-!- SUBUNIT: Forms homodimer or heterodimer with other members of the
family.
CC
CC -!- SIMILARITY: Belongs to the TPD52 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U44427; AAB40894.1; -.
CC MGI; U44428; AAB40895.1; -.
CC Genew; HGNC:12006; TPD52L1.
CC MIM: 604069; -.
CC InterPro; IPR007327; TPD52.
CC Pfam; PF04201; TPD52; 1.
CC Coiled coil. 22 73 COILED COIL (POTENTIAL).
CC DOMAIN 22 73 COILED COIL (POTENTIAL).
CC SEQUENCE 204 AA; 22449 MW; 6B3C36D5C0653C9 CRC64;
FT FT
SQ

Query Match 3.6%; Score 7; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194
DB 33 EEEKEEL 39

RESULT 10
TPD53 MOUSE STANDARD; PRT; 204 AA.
ID ID TPDS3 MOUSE STANDARD; PRT; 210 AA.
AC AC Q918F4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Tumor protein D53 homolog.
GN TPDS2L1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBUNIT: Forms homodimer or heterodimer with other members of the
CC family (By similarity).
CC -!- SIMILARITY: Belongs to the TPD52 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY004870; AAF87084.1; -.
CC InterPro; IPR007327; TPD52.
CC Pfam; PF04201; TPD52; 1.
CC Coiled coil. 22 73 COILED COIL (POTENTIAL).
CC DOMAIN 22 73 COILED COIL (POTENTIAL).
CC SEQUENCE 210 AA; 23253 MW; 73AFD4255165A5A6 CRC64;
FT FT
SQ

Query Match 3.6%; Score 7; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Sadow P.W., Hanna M.C.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Fodor S.P., Nguyen D.,
RA Coton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Frazer C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- FUNCTION: Ribosomal protein P0 is the functional equivalent of
CC E.coli protein L10.
CC -!- SIMILARITY: Belongs to the L10P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67500; AAB98499.1; -
DR TIGR; M70509; -
DR HAMAP; MF_00280; -; 1.
DR InterPro; IPR001790; Ribosomal L10.
DR Pfam; PF0466; Ribosomal L10; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 338 AA; 36751 MW; 63A6AFD357E3052D CRC64;

Query Match 3.6%; Score 7; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 22; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 187 ABEKEE 193
Db 311 ABEKEE 317

RESULT 14
MSME STRMU STANDARD; PRT; 420 AA.
AC Q00749; 1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Multiple sugar-binding protein precursor.
GN MSME OR SMU-878.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ingbritt;
RX MEDLINE=92165821; PubMed=1537846;
RA Russell R.R.B., Aduse-Opoku J., Sutcliffe I.C., Tao L.,
RA Ferretti J.J.;
RT "A binding protein-dependent transport system in Streptococcus mutans
RT responsible for multiple sugar metabolism."
RL J. Biol. Chem. 267:4631-4637(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RX Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,

```

RL Nature 323:461-464 (1986).  
CC -!- FUNCTION: Removes residual C-terminal Arg or Lys remaining after  
CC initial endoprotease cleavage during prohormone processing.  
CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysine (or L-arginine) + H(2)O =  
CC peptide + L-lysine (or L-arginine).  
CC -!- SUBCELLULAR LOCATION: Secretory granules of pancreatic islets,  
CC adrenal gland, pituitary and brain.  
CC -!- SIMILARITY: Belongs to peptidase family M14.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X04411; CAA27999.1; -.  
CC PIR; A24327; A24327.  
CC MEROPS; M14.005; -.  
CC InterPro; IPR008969; Carboxypeptidase\_M14.  
CC InterPro; IPR008969; Peptidase\_M14.  
CC InterPro; IPR008969; Peptidase\_M14B.  
CC Pfam; PF05885; DUF857; 1.  
CC Pfam; PF00246; Zn\_carboxypept; 1.  
CC PRINTS; PR00765; CRBOXYPEPTASE.  
CC SMART; SM00631; Zn\_pept; 1.  
CC PROSITE; PS00132; CARBOXYPEPT\_ZN\_1; 1.  
CC PROSITE; PS00133; CARBOXYPEPT\_ZN\_2; 1.  
CC KX Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Glycoprotein.  
FT METAL 72 75  
FT METAL 75 75  
FT ACT SITE 206 206  
FT ACT SITE 300 300  
FT CARBOHYD 97 97  
FT CARBOHYD 348 348  
FT SEQUENCE 434 AA; 49205 MW; E1E848FE5139DBED CRC64;  
Query Match 3.6%; Score 7; DB 1; Length 434;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 188 EEEKEEL 194  
DB 415 EEEKEEL 421

Search completed: May 17, 2004, 10:51:51  
Job time : 48 secs

Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;  
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
pathogen.";  
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).  
-!- FUNCTION: Involved in a binding protein-dependent transport system  
responsible for the uptake of melibiose, raffinose and  
isomaltotriose.  
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
(Probable).  
-!- INDUCTION: By raffinose.  
-!- SIMILARITY: Belongs to the bacterial extracellular solute-binding  
protein family 1.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M77351; AAA26934.1; -.  
CC EMBL; AE014929; AAN58593.1; -.  
CC PIR; B42400; B42400.  
CC InterPro; IPR000437; Prok\_lipoprot\_S.  
CC InterPro; IPR006059; SBP\_bac1.  
CC InterPro; IPR006061; SBP\_dom1.  
CC Pfam; PF01547; SBP\_bac1; 1.  
CC PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
CC PROSITE; PS01037; SBP\_BACTERIAL\_1; 1.  
CC TRANSPORT; Sugar transport; Lipoprotein; Membrane; Signal;  
CC Complete proteome; Palmitate.  
CC SIGNAL 1 22  
CC CHAIN 23 420 MULTIPLE SUGAR-BINDING PROTEIN.  
CC LIPID 23 23 N-palmitoyl cysteine (Probable).  
CC LIPID 23 23 S-diacylglycerol cysteine (Probable).  
CC CONFLICT 27 28 KA -> NG (IN REF. 1).  
CC CONFLICT 33 33 E -> D (IN REF. 1).  
CC CONFLICT 277 287 ALPAKQDDPK -> PCOLLNNKIPN (IN REF. 1).  
CC CONFLICT 372 372 D -> H (IN REF. 1).  
CC CONFLICT 388 388 F -> L (IN REF. 1).  
CC SEQUENCE 420 AA; 47087 MW; FA7CF7AECG3DEFA7 CRC64;  
Query Match 3.6%; Score 7; DB 1; Length 420;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 93 LGLKVPE 99  
DB 158 LGLKVPE 164

RESULT 15  
CBPH BOVIN STANDARD; PRT; 434 AA.  
AC P04836;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Carboxypeptidase H (EC 3.4.17.10) (CPH) (Carboxypeptidase E) (CPE)  
DE (Enkephalin convertase) (Prohormone processing carboxypeptidase).  
GN CPE.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OC NCBI TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87014809; PubMed=3020433;  
RA Fricker L.D., Evans C.J., Esch F.S., Herbert E.;  
RT "Cloning and sequence analysis of cDNA for bovine carboxypeptidase  
E.";

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

MM protein - protein search, using sw model

Run on: May 17, 2004, 10:48:10 ; Search time 45 Seconds  
(without alignments)  
1360.234 Million cell updates/sec

Title: US-10-621-401-145  
Perfect score: 194  
Sequence: 1 MLAGFLVLSLGGGLAQ.....PFMNSQRAACICAEKEEL 194

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rhod:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	19.6	195	11 Q8VC81	Q8VC81 mus musculus
2	13	6.7	180	13 Q7ZYI1	Q7ZYI1 brachydanio
3	8	4.1	321	16 Q8XGL7	Q8XGL7 ralstonia s
4	8	4.1	484	16 Q82B38	Q82B38 streptomyce
5	8	4.1	489	16 Q9L004	Q9L004 streptomyce
6	8	4.1	497	16 Q7WL74	Q7WL74 bordetella
7	8	4.1	497	16 Q7W7T4	Q7W7T4 bordetella
8	8	4.1	497	16 Q7VWF4	Q7VWF4 bordetella
9	8	4.1	528	10 Q9C6J7	Q9C6J7 arabidopsis
10	8	4.1	603	16 Q899H3	Q899H3 clostridium
11	8	4.1	637	3 Q9Y815	Q9Y815 schizosacch
12	8	4.1	768	10 Q9C6J6	Q9C6J6 arabidopsis
13	8	4.1	5035	11 Q80X16	Q80X16 mus musculus
14	7	3.6	49	16 Q984N0	Q984N0 mus musculus
15	7	3.6	63	16 Q8YMR5	Q8YMR5 anabaena sp
16	7	3.6	75	17 Q97ZP8	Q97ZP8 sulfolobus

17	3.6	75	17	Q97XE7	Q97XE7 sulfolobus
18	3.6	88	2	Q9L9D8	Q9L9D8 bordetella
19	3.6	88	16	Q84CR2	Q84CR2 bordetella
20	3.6	91	16	Q7WLW2	Q7WLW2 bordetella
21	3.6	91	16	Q7W8A3	Q7W8A3 bordetella
22	3.6	103	4	Q9NNZ6	Q9NNZ6 homo sapien
23	3.6	106	3	Q9HFQ7	Q9HFQ7 candida alb
24	3.6	106	3	Q94018	Q94018 candida alb
25	3.6	110	2	Q939G1	Q939G1 pseudomonas
26	3.6	111	3	Q9HFQ4	Q9HFQ4 candida alb
27	3.6	124	16	Q82Q59	Q82Q59 streptomyce
28	3.6	131	4	Q9C054	Q9C054 homo sapien
29	3.6	133	10	Q7XY30	Q7XY30 griffithsia
30	3.6	144	4	Q9BU06	Q9BU06 homo sapien
31	3.6	144	4	O43397	O43397 homo sapien
32	3.6	158	16	Q92P52	Q92P52 rhizobium m
33	3.6	168	16	Q8XQG1	Q8XQG1 ralstonia s
34	3.6	174	16	Q83AR0	Q83AR0 coxiella bu
35	3.6	182	12	Q7T4F6	Q7T4F6 pike fry-li
36	3.6	182	12	Q7T4F5	Q7T4F5 pike fry-li
37	3.6	182	12	Q7T4F4	Q7T4F4 pike fry-li
38	3.6	182	12	Q7T4F3	Q7T4F3 pike fry-li
39	3.6	182	12	Q7T4F2	Q7T4F2 pike fry-li
40	3.6	182	12	Q7T4E4	Q7T4E4 pike fry-li
41	3.6	182	12	Q7T4E3	Q7T4E3 pike fry-li
42	3.6	182	12	Q7T4E2	Q7T4E2 pike fry-li
43	3.6	182	12	Q7T4E1	Q7T4E1 pike fry-li
44	3.6	182	12	Q7T4E0	Q7T4E0 pike fry-li
45	3.6	182	12	Q7T4D9	Q7T4D9 pike fry-li
46	3.6	182	12	Q7T4D8	Q7T4D8 pike fry-li
47	3.6	182	12	Q7T4D7	Q7T4D7 pike fry-li
48	3.6	182	12	Q7T4D6	Q7T4D6 pike fry-li
49	3.6	182	12	Q7T4D5	Q7T4D5 pike fry-li
50	3.6	182	12	Q7T4D4	Q7T4D4 pike fry-li
51	3.6	182	12	Q7T4D3	Q7T4D3 pike fry-li
52	3.6	182	12	Q7T4D2	Q7T4D2 pike fry-li
53	3.6	182	12	Q7T4D1	Q7T4D1 pike fry-li
54	3.6	182	12	Q7T4D0	Q7T4D0 pike fry-li
55	3.6	191	10	Q82809	Q82809 arabidopsis
56	3.6	191	10	Q8LDX1	Q8LDX1 arabidopsis
57	3.6	191	10	O04154	O04154 arabidopsis
58	3.6	212	12	Q91TR8	Q91TR8 tupaia herp
59	3.6	241	2	O51308	O51308 nitrosospi
60	3.6	243	4	Q86X76	Q86X76 homo sapien
61	3.6	244	16	Q836D4	Q836D4 enterococcu
62	3.6	255	2	O54889	O54889 serratia pr
63	3.6	258	3	Q93871	Q93871 verricillu
64	3.6	260	16	Q82HP0	Q82HP0 streptomyce
65	3.6	270	17	Q8PWH1	Q8PWH1 methanosarc
66	3.6	277	10	Q8S253	Q8S253 oryza sativ
67	3.6	287	16	Q8D104	Q8D104 yersinia pe
68	3.6	288	13	Q918G0	Q918G0 xenopus lae
69	3.6	293	16	Q7UJF6	Q7UJF6 rhodospirell
70	3.6	298	5	Q20193	Q20193 caenorhabdi
71	3.6	300	5	Q9N8B3	Q9N8B3 trypanosoma
72	3.6	303	2	Q9R3A7	Q9R3A7 escherichia
73	3.6	304	2	Q53792	Q53792 streptomyce
74	3.6	309	16	Q82VR6	Q82VR6 nitrosomona
75	3.6	312	16	Q8PA20	Q8PA20 xanthomonas
76	3.6	314	3	Q9C3Z6	Q9C3Z6 podospora a
77	3.6	317	16	Q8UBZ1	Q8UBZ1 agrobacteri
78	3.6	320	2	Q8RKT9	Q8RKT9 serratia ma
79	3.6	320	2	Q9X9D8	Q9X9D8 serratia sp
80	3.6	320	16	Q82D83	Q82D83 yersinia pe
81	3.6	324	2	O85477	O85477 yersinia en
82	3.6	326	2	O68878	O68878 pseudomonas
83	3.6	327	4	O76091	O76091 homo sapien
84	3.6	327	16	Q9HV91	Q9HV91 pseudomonas
85	3.6	337	2	Q8GL33	Q8GL33 borrelia bu
86	3.6	343	2	Q9S035	Q9S035 borrelia bu
87	3.6	348	13	Q7SZ21	Q7SZ21 xenopus lae
88	3.6	363	5	Q9N4W7	Q9N4W7 caenorhabdi
89	3.6	380	17	Q8Z2C8	Q8Z2C8 pyrobaculum



90	7	3.6	388	5	Q9N888	Q9n888 plasmodium	163	7	3.6	1231	5	Q24098	Q24098 drosophila
91	7	3.6	395	16	Q8PIL0	Q8p110 xanthomonas	164	7	3.6	1294	16	Q8PKH5	Q8pkhs xanthomonas
92	7	3.6	398	16	Q8P710	Q8p791 xanthomonas	165	7	3.6	1305	3	Q9P424	Q9p424 ajellomyces
93	7	3.6	412	12	Q9QH54	Q9qh54 gallid herp	166	7	3.6	1318	16	Q7UG24	Q7ug24 rhodopirell
94	7	3.6	418	10	Q64517	Q64517 arabidopsis	167	7	3.6	1381	11	Q8CGE9	Q8cge9 mus musculus
95	7	3.6	418	10	Q7XB11	Q7xb11 arabidopsis	168	7	3.6	1548	10	Q85531	Q85531 arabidopsis
96	7	3.6	419	16	Q97NW2	Q97nw2 streptococ	169	7	3.6	1846	4	Q86YS8	Q86ys8 homo sapien
97	7	3.6	419	16	Q8DNH8	Q8dnh8 streptococ	170	7	3.6	2109	5	Q8IAS7	Q8ias7 plasmodium
98	7	3.6	442	4	Q8N7F2	Q8n7f2 homo sapien	171	7	3.6	2515	5	Q24551	Q24551 drosophila
99	7	3.6	448	16	Q9KPF8	Q9kpf8 bacillus ha	172	7	3.6	2731	5	Q9VNU6	Q9vnu6 drosophila
100	7	3.6	451	16	Q5O870	Q5o870 borrelia bu	173	7	3.6	2731	5	Q61307	Q61307 drosophila
101	7	3.6	460	17	Q58649	Q58649 pyrococcus	174	7	3.6	2731	5	Q18366	Q18366 drosophila
102	7	3.6	464	17	Q9U2B9	Q9u2b9 pyrococcus	175	7	3.6	4163	2	Q9LAE6	Q9lae6 rhizobium l
103	7	3.6	465	17	Q85724	Q85724 streptomyce	176	7	3.6	4730	5	Q8T128	Q8t128 dictyosteli
104	7	3.6	489	2	Q85724	Q85724 streptomyce	177	6	3.1	21	21	Q9R5U9	Q9r5u9 rhodococcus
105	7	3.6	502	4	Q9H925	Q9h925 homo sapien	178	6	3.1	28	2	Q50102	Q50102 mycobacteri
106	7	3.6	519	10	Q9CAD4	Q9cad4 arabidopsis	179	6	3.1	31	11	Q8CGM7	Q8cgm7 mus musculu
107	7	3.6	523	2	Q54200	Q54200 streptomyce	180	6	3.1	31	11	Q8H9K8	Q8h9k8 vibrio harv
108	7	3.6	539	11	Q9Z1J7	Q9z1j7 rattus norv	181	6	3.1	49	9	Q8H9K8	Q8h9k8 human herpe
109	7	3.6	540	10	Q8LCK4	Q8lck4 arabidopsis	182	6	3.1	50	12	Q8V270	Q8v270 human herpe
110	7	3.6	540	10	Q8W469	Q8w469 arabidopsis	183	6	3.1	53	2	Q93A11	Q93a11 thiobacillu
111	7	3.6	547	10	Q8SFV1	Q8sfv1 arabidopsis	184	6	3.1	54	16	Q7UYJ1	Q7uyj1 rhodopirell
112	7	3.6	548	16	Q8FOP9	Q8fop9 corynebacte	185	6	3.1	57	17	Q8PZF5	Q8pzf5 methanosarc
113	7	3.6	564	5	Q9V369	Q9v369 drosophila	186	6	3.1	59	9	Q9MCE5	Q9mcb5 lactococcus
114	7	3.6	619	4	Q73453	Q73453 homo sapien	187	6	3.1	60	10	Q9LJD9	Q9ljd9 arabidopsis
115	7	3.6	632	10	Q9C6K1	Q9c6k1 arabidopsis	188	6	3.1	60	10	Q9LJD9	Q9ljd9 mus musculu
116	7	3.6	649	4	Q86PL7	Q86pl7 homo sapien	189	6	3.1	62	11	Q9CSJ9	Q9csg9 lactococcus
117	7	3.6	650	4	Q81YX9	Q81yx9 homo sapien	190	6	3.1	62	16	Q9CG40	Q9cg40 lactococcus
118	7	3.6	652	4	Q88357	Q88357 homo sapien	191	6	3.1	67	16	Q7UEY9	Q7uey9 rhodopirell
119	7	3.6	653	6	Q95L97	Q95l97 felis silve	192	6	3.1	68	16	Q8R7Q8	Q8r7q8 thermoaer
120	7	3.6	666	10	Q8RXC3	Q8rxc3 arabidopsis	193	6	3.1	70	16	Q8R9Q3	Q8rgq3 bradyrhizob
121	7	3.6	677	16	Q9KAS2	Q9kas2 bacillus ha	194	6	3.1	71	5	Q93186	Q93186 caenorhabdi
122	7	3.6	678	2	Q9K114	Q9k114 mycobacteri	195	6	3.1	73	5	Q8T844	Q8t844 dictyosteli
123	7	3.6	678	8	Q7YJX9	Q7y1x9 calycanthus	196	6	3.1	73	16	Q7UX55	Q7ux55 rhodopirell
124	7	3.6	687	2	Q8KU02	Q8ku02 listeria mo	197	6	3.1	74	7	P79637	P79637 oncorhynch
125	7	3.6	722	13	Q9W6K6	Q9w6k6 salmo salar	198	6	3.1	75	11	Q8VEI7	Q8vei7 mus musculu
126	7	3.6	723	11	Q9D677	Q9d677 mus musculu	199	6	3.1	75	12	O57140	O57140 human herpe
127	7	3.6	725	4	Q86WM9	Q86wm9 homo sapien	200	6	3.1	76	7	Q951W9	Q951w9 oncorhynch
128	7	3.6	732	4	Q9H7P8	Q9h7p8 homo sapien	201	6	3.1	79	12	Q96895	Q96895 human herpe
129	7	3.6	734	16	Q8XN26	Q8xn26 clostridium	202	6	3.1	80	17	Q9HHP8	Q9hnp8 halobacteri
130	7	3.6	736	2	P77038	P77038 escherichia	203	6	3.1	82	9	Q853Y6	Q853y6 mycobacteri
131	7	3.6	753	16	Q7UHR1	Q7uhr1 rhodopirell	204	6	3.1	82	16	Q8PFE2	Q8pfe2 xanthomonas
132	7	3.6	759	4	Q9NW13	Q9nw13 homo sapien	205	6	3.1	84	16	Q8UBK9	Q8ubk9 agrobacteri
133	7	3.6	759	4	Q86CV3	Q86cv3 homo sapien	206	6	3.1	86	1	Q8U750	Q8u750 methanobact
134	7	3.6	771	4	Q96C12	Q96c12 homo sapien	207	6	3.1	86	5	Q8T5K9	Q8t5k9 anopheles g
135	7	3.6	780	10	Q9SA10	Q9sa10 arabidopsis	208	6	3.1	86	6	Q8HZZ8	Q8hzz8 macaca fasc
136	7	3.6	783	10	Q9FVX6	Q9fvx6 arabidopsis	209	6	3.1	89	10	Q42367	Q42367 zea mays (m
137	7	3.6	788	4	Q8TDO5	Q8tdq5 homo sapien	210	6	3.1	89	10	Q42368	Q42368 zea mays (m
138	7	3.6	791	4	Q9V4S4	Q9v4s4 homo sapien	211	6	3.1	90	10	Q8H4N9	Q8h4n9 oryza sativ
139	7	3.6	812	10	Q9C6J9	Q9c6j9 arabidopsis	212	6	3.1	91	16	Q8ER66	Q8er66 oceanobacil
140	7	3.6	816	16	Q9CHS9	Q9chs9 lactococcus	213	6	3.1	92	10	Q9LGS9	Q9lgs9 oryza sativ
141	7	3.6	822	16	Q8EUA6	Q8eua6 mycoplasma	214	6	3.1	93	13	Q801B3	Q801b3 latimeria m
142	7	3.6	832	10	Q9SLE5	Q9sle5 arabidopsis	215	6	3.1	94	12	Q8JQM5	Q8jqm5 human herpe
143	7	3.6	848	10	Q9SCU9	Q9scu9 arabidopsis	216	6	3.1	94	12	Q8JQM1	Q8jqm1 human herpe
144	7	3.6	851	16	Q91442	Q91442 pseudomonas	217	6	3.1	95	16	Q7UUM1	Q7uum1 rhodopirell
145	7	3.6	879	10	Q82177	Q82177 arabidopsis	218	6	3.1	95	17	Q8PXF7	Q8pxp7 methanosarc
146	7	3.6	896	5	Q19370	Q19370 caenorhabdi	219	6	3.1	96	16	Q82QH0	Q82qh0 streptomyce
147	7	3.6	900	10	Q23454	Q23454 arabidopsis	220	6	3.1	97	10	Q04816	Q04816 sporobolus
148	7	3.6	931	5	Q9VVU6	Q9vvu6 drosophila	221	6	3.1	97	13	Q90XG3	Q90xg3 gallus gall
149	7	3.6	962	10	Q84KL1	Q84kl1 cyanidiosch	222	6	3.1	98	16	Q7VKK5	Q7vkk5 haemophilus
150	7	3.6	962	16	Q837Q7	Q837q7 enterococcu	223	6	3.1	99	17	Q26906	Q26906 methanobact
151	7	3.6	1041	12	Q9ELF7	Q9elf7 meleagrid h	224	6	3.1	100	2	O52301	O52301 escherichia
152	7	3.6	1041	12	Q9DPQ2	Q9dpq2 meleagrid h	225	6	3.1	100	2	O52302	O52302 escherichia
153	7	3.6	1054	5	Q8IR12	Q8ir12 drosophila	226	6	3.1	100	2	O52303	O52303 escherichia
154	7	3.6	1126	11	Q8BHP2	Q8bhp2 mus musculu	227	6	3.1	100	2	O52303	O52303 escherichia
155	7	3.6	1132	4	Q86Y26	Q86y26 homo sapien	228	6	3.1	100	16	Q89AT7	Q89at7 buchnera ap
156	7	3.6	1137	5	Q9V649	Q9v649 drosophila	229	6	3.1	101	11	Q8BMV6	Q8bm6 mus musculu
157	7	3.6	1146	5	Q8MRD5	Q8mrd5 drosophila	230	6	3.1	101	12	Q8JMC8	Q8jmc8 mamestra co
158	7	3.6	1200	5	Q9VXE9	Q9vxe9 drosophila	231	6	3.1	104	17	Q96Z31	Q96z31 sulfolobus
159	7	3.6	1201	5	Q81952	Q8i952 anopheles g	232	6	3.1	105	17	Q8TJZ7	Q8tzj7 pyrococcus
160	7	3.6	1217	4	Q86VX4	Q86vx4 homo sapien	233	6	3.1	107	10	Q8W332	Q8w332 oryza sativ
161	7	3.6	1217	13	Q8AWB8	Q8awb8 gallus gall	234	6	3.1	108	11	Q8C6T8	Q8c6t8 mus musculu
162	7	3.6	1217	13	Q8AW91	Q8aw91 xenopus lae	235	6	3.1	109	3	Q8TFM9	Q8tfm9 fusarium cu

236	6	3.1	109	10	Q8LBM7	Q8lbm7 arabidopsis	309	6	3.1	144	8	Q9TJ22	Q9Tcj22 arabidopsis
237	6	3.1	110	2	Q3VQR3	Q3vqr3 escherichia	310	6	3.1	144	16	Q8YM42	Q8ym42 anabaena sp
238	6	3.1	110	2	Q3VNS4	Q3vns4 escherichia	311	6	3.1	145	11	Q8CD69	Q8cd69 mus musculus
239	6	3.1	110	9	Q80048	Q80048 staphylococ	312	6	3.1	146	2	Q9R8B8	Q9r8b8 pseudomonas
240	6	3.1	110	9	Q8SDK7	Q8sdk7 staphylococ	313	6	3.1	146	2	Q9X6F3	Q9x6f3 pseudomonas
241	6	3.1	110	11	Q8CDK16	Q8cdk16 mus musculus	314	6	3.1	148	10	Q9M4E1	Q9m4e1 avena sativ
242	6	3.1	110	16	Q8CNVQ0	Q8cnvq0 staphylococ	315	6	3.1	149	16	Q8ZCA9	Q8zca9 yersinia pe
243	6	3.1	110	16	Q7UII7	Q7uit7 rhodopirell	316	6	3.1	149	16	Q7UXE1	Q7uxel rhodopirell
244	6	3.1	110	17	Q8TTB3	Q8ttb3 methanosarc	317	6	3.1	149	17	Q8TW19	Q8tw19 methanopyru
245	6	3.1	111	3	Q8HGV0	Q8hgv0 aspergillus	318	6	3.1	150	16	Q8XEN4	Q8xen4 salmonella
246	6	3.1	111	3	Q8HGU9	Q8hgu9 aspergillus	319	6	3.1	150	16	Q8ZQI1	Q8zqi1 streptomyce
247	6	3.1	111	3	Q9C3Z5	Q9c3z5 podospora a	320	6	3.1	151	10	Q8FGU8	Q8fgu8 arabidopsis
248	6	3.1	111	17	Q8ZX60	Q8zx60 pyrobaculum	321	6	3.1	151	10	Q8LB92	Q8lb92 arabidopsis
249	6	3.1	112	6	Q46478	Q46478 oryctolagus	322	6	3.1	151	12	Q6S866	Q6s866 barley yell
250	6	3.1	113	5	Q9NIV6	Q9niv6 tegula mont	323	6	3.1	151	16	Q8XD05	Q8xd05 escherichia
251	6	3.1	113	9	Q9MBP8	Q9mbp8 staphylococ	324	6	3.1	152	2	Q8KV49	Q8kv49 escherichia
252	6	3.1	113	16	Q8D3A4	Q8d3a4 wigglewort	325	6	3.1	152	2	Q8FK72	Q8fk72 escherichia
253	6	3.1	114	10	Q8LLC1	Q8llcl hordeum vul	326	6	3.1	152	16	Q8FDX9	Q8fdx9 escherichia
254	6	3.1	114	10	Q8LUK2	Q8luk2 arabidopsis	327	6	3.1	152	16	Q7VE00	Q7ve00 prochloroco
255	6	3.1	114	16	Q8PGG6	Q8pgg6 xanthomonas	328	6	3.1	155	2	Q8XQ32	Q8xq32 pseudomonas
256	6	3.1	115	5	Q8IFK4	Q8ifk4 riftia pach	329	6	3.1	155	17	Q8FVH8	Q8fvh8 methanosarc
257	6	3.1	115	11	Q8CAME6	Q8cam6 mus musculus	330	6	3.1	156	5	Q9XTZ7	Q9xtz7 caenorhabdi
258	6	3.1	115	16	Q7V2D9	Q7v2d9 prochloroco	331	6	3.1	157	11	Q8BHZ5	Q8bh25 mus musculus
259	6	3.1	116	8	Q97TK2	Q97tk2 crassostrea	332	6	3.1	157	11	Q8G3L9	Q8gpl9 methylobact
260	6	3.1	116	10	Q8GS81	Q8gs81 oryza sativ	333	6	3.1	158	2	Q8G3L9	Q8siu8 oryza sativ
261	6	3.1	116	16	Q8ETA7	Q8eta7 oceanobacil	334	6	3.1	158	10	Q8S1U8	Q8s1u8 salmonella
262	6	3.1	117	8	O19962	O19962 gossypium a	335	6	3.1	158	16	Q934V0	Q934v0 raistonia s
263	6	3.1	117	8	O19963	O19963 gossypium h	336	6	3.1	160	5	Q86BH9	Q86eh9 schistosoma
264	6	3.1	117	8	O19966	O19966 gossypium m	337	6	3.1	161	4	Q7Z5K0	Q7z5k0 homo sapien
265	6	3.1	117	8	O19964	O19964 gossypium b	338	6	3.1	161	12	Q8UZD3	Q8uzd3 cercopithic
266	6	3.1	117	8	O19967	O19967 gossypium d	339	6	3.1	162	16	Q8B248	Q8b248 xanthomonas
267	6	3.1	117	8	O19965	O19965 gossypium t	340	6	3.1	163	16	Q8B7U0	Q8b7u0 pyrococcus
268	6	3.1	118	5	Q8I3S2	Q8i3s2 plasmodium	341	6	3.1	164	10	Q94AA2	Q94aa2 arabidopsis
269	6	3.1	118	8	O20422	O20422 diphylobot	342	6	3.1	164	16	Q88NT4	Q88nt4 pseudomonas
270	6	3.1	120	12	Q69247	Q69247 bovine herp	343	6	3.1	165	16	Q87XQ0	Q87xq0 pseudomonas
271	6	3.1	120	16	Q8Z1J8	Q8zi18 salmonella	344	6	3.1	165	16	Q87XQ0	Q87xq0 pseudomonas
272	6	3.1	121	10	Q9SDS0	Q9eds0 prunus dulc	345	6	3.1	168	11	Q9JXF2	Q9jxf2 mus musculus
273	6	3.1	122	2	Q9FAP2	Q9faf2 bacillus au	346	6	3.1	168	11	Q9JXF2	Q9jxf2 mus musculus
274	6	3.1	122	16	Q8R7M0	Q8r7m0 thermoanaer	347	6	3.1	168	12	Q9MXJ8	Q9mxj8 hepatitis e
275	6	3.1	123	16	Q8F6B4	Q8f6e4 leptospira	348	6	3.1	168	16	Q9CP78	Q9cp78 pasteurella
276	6	3.1	124	16	Q8BPC1	Q8bpcl pseudomonas	349	6	3.1	170	16	Q9Z956	Q9z956 chlamydia p
277	6	3.1	124	16	Q7U9P0	Q7u9p0 pectinopygu	350	6	3.1	171	10	Q9FWH2	Q9fhw2 arabidopsis
278	6	3.1	126	8	Q7YBU7	Q7ybu7 lactobacill	351	6	3.1	172	4	Q9UL45	Q9ul45 homo sapien
279	6	3.1	126	9	Q9TIF5	Q9tif5 corynebacte	352	6	3.1	172	5	Q7VTR8	Q7vtr8 caenorhabdi
280	6	3.1	126	16	Q8FTD1	Q8ftd1 corynebacte	353	6	3.1	172	11	Q9ROC0	Q9roc0 mus musculus
281	6	3.1	127	5	Q8SUJ0	Q8suj0 encephalito	354	6	3.1	172	16	Q7TIW1	Q7tw1 synchococc
282	6	3.1	129	16	Q8YRV1	Q8yrv1 anabaena sp	355	6	3.1	172	8	Q8HMB1	Q8hm81 lota lota (
283	6	3.1	130	16	Q8ZDF0	Q8zdf0 anabaena sp	356	6	3.1	173	8	Q8HKL1	Q8hkl1 suiffamen f
284	6	3.1	131	10	Q94HR0	Q94hr0 oryza sativ	357	6	3.1	173	16	Q81GT2	Q81gt2 bacillus ce
285	6	3.1	131	10	Q9XFU4	Q9xfu4 oryza sativ	358	6	3.1	174	16	Q81GT2	Q81gt2 bacillus ce
286	6	3.1	131	17	Q9VOT3	Q9vot3 pyrococcus	359	6	3.1	175	8	Q99605	Q99605 artibeus ja
287	6	3.1	131	17	Q973M6	Q973w6 sulfolobus	360	6	3.1	175	10	Q8S1Z3	Q8s1z3 oryza sativ
288	6	3.1	132	10	Q8SAA6	Q8saa6 arabidopsis	361	6	3.1	175	11	Q9JXF3	Q9jxf3 mus musculus
289	6	3.1	132	10	Q7XJY0	Q7xjy0 oryza sativ	362	6	3.1	175	16	Q8XU18	Q8xul8 ralstonia s
290	6	3.1	132	16	Q81KR6	Q81kr6 bacillus an	363	6	3.1	176	2	Q9EVH8	Q9ev88 clostridium
291	6	3.1	132	16	Q816Z0	Q816z0 bacillus ce	364	6	3.1	176	4	Q9BQD3	Q9bqd3 homo sapien
292	6	3.1	132	16	Q7UR18	Q7ur18 rhodopirell	365	6	3.1	176	5	Q9VKY6	Q9vky6 drosophila
293	6	3.1	133	5	Q9NIV7	Q9niv7 tegula brun	366	6	3.1	176	5	Q9VTC9	Q9vtc9 drosophila
294	6	3.1	133	8	Q36413	Q36413 lachnaia sp	367	6	3.1	177	11	Q80XH1	Q80xh1 mus musculus
295	6	3.1	133	10	Q7XUI3	Q7xui3 oryza sativ	368	6	3.1	177	11	Q80XH1	Q80xh1 mus musculus
296	6	3.1	134	16	Q7UVV4	Q7uvv4 rhodopirell	369	6	3.1	178	16	Q8NNV5	Q8nnv5 corynebacte
297	6	3.1	134	17	Q8PWB8	Q8pwb8 methanosarc	370	6	3.1	178	17	Q58005	Q58005 pyrococcus
298	6	3.1	135	5	Q86KV4	Q86kv4 dictyosteli	371	6	3.1	179	4	Q7Z4E2	Q7z4e2 homo sapien
299	6	3.1	135	17	Q96Z82	Q96z82 sulfolobus	372	6	3.1	180	5	Q27357	Q27357 bradyasia hy
300	6	3.1	136	5	Q7YWB5	Q7ywb5 ixodes rici	373	6	3.1	180	5	Q27357	Q27357 bradyasia hy
301	6	3.1	136	16	Q8ZHH1	Q8zh1 yersinia pe	374	6	3.1	181	11	Q8BPJ0	Q8bpj0 mus musculus
302	6	3.1	136	16	Q8DHG6	Q8dhg6 synchococc	375	6	3.1	181	16	Q8ZAB7	Q8za87 listeria in
303	6	3.1	138	16	Q8ERQ6	Q8erq6 oceanobacil	376	6	3.1	181	16	Q8ZY07	Q8zy07 nitrosomona
304	6	3.1	140	8	Q85FP8	Q85fp8 cyanidiosch	377	6	3.1	182	4	Q8WXX8	Q8wx88 homo sapien
305	6	3.1	141	11	Q8BQK3	Q8bqk3 mus musculus	378	6	3.1	182	4	Q86DF4	Q86df4 heterodera
306	6	3.1	142	2	O87513	O87513 escherichia	379	6	3.1	183	4	Q76098	Q76098 homo sapien
307	6	3.1	142	11	Q8C7N3	Q8c7n3 mus musculus	380	6	3.1	183	16	Q8R7D1	Q8r7d1 thermoanaer
308	6	3.1	143	16	Q9ZKT3	Q9zkt3 helicobacte	381	6	3.1	184	6	Q9T506	Q9t506 oryctolagus

382	6	3.1	184	9	Q9MC20	Q9mc20 lactococcus	455	206	16	Q9RWY4	Q9rwy4 deinococcus
383	6	3.1	184	16	Q910K2	Q910k2 pseudomonas	456	206	17	Q8U0M1	Q8u0m1 pyrococcus
384	6	3.1	185	5	Q22660	Q22660 caenorhabdi	457	206	17	Q8THG9	Q8thg9 methanosarc
385	6	3.1	185	5	Q86M77	Q86m77 heterodera	458	206	17	Q8PXH6	Q8pxh6 methanosarc
386	6	3.1	185	10	Q9MA15	Q9ma15 arabidopsis	459	208	10	Q9LGS1	Q9lgs1 oryza sativ
387	6	3.1	185	11	Q8C4A9	Q8c4a9 mus musculu	460	208	10	Q8S6A3	Q8s6a3 oryza sativ
388	6	3.1	185	11	Q8BNX6	Q8bnx6 mus musculu	461	208	11	Q9CVW7	Q9cvw7 mus musculu
389	6	3.1	185	17	Q8PNW6	Q8pnw6 methanosarc	462	208	12	Q8XJBO	Q8xjbo clostridium
390	6	3.1	186	10	Q9ZQH1	Q9zqni arabidopsis	463	208	12	Q91FL9	Q91fl9 chilo iride
391	6	3.1	186	16	Q9CNZ9	Q9cnz9 pasteurilla	464	208	16	Q8NZL6	Q8nzb6 streptococ
392	6	3.1	187	16	Q8EBI8	Q8ebi8 shewanella	465	208	17	Q970I9	Q970i9 sulfolobus
393	6	3.1	187	16	Q7ZAN2	Q7zan2 corynebacte	466	209	11	Q9UKF4	Q9ukf4 mus musculu
394	6	3.1	188	2	Q52933	Q52933 rhizobium m	467	210	2	Q9XKZ9	Q9xkz9 streptococ
395	6	3.1	188	6	Q9GME4	Q9gme4 callithrix	468	210	16	Q9A6K8	Q9a6k8 caulobacter
396	6	3.1	188	16	P74118	P74118 synecocyst	469	211	16	Q82BJ5	Q82bj5 streptomyce
397	6	3.1	189	5	Q8IC97	Q8ic97 plasmodium	470	211	5	Q93TE9	Q93te9 pseudomonas
398	6	3.1	189	11	Q7TWG5	Q7twg5 mus musculu	471	211	21	Q93TE9	Q93te9 caenorhabdi
399	6	3.1	190	4	Q86WE3	Q86we3 homo sapien	472	211	21	Q93TE9	Q93te9 cucumis sat
400	6	3.1	190	11	P70456	P70456 mus musculu	473	211	10	Q92TQ9	Q92tq9 arabidopsis
401	6	3.1	191	12	Q99FP5	Q99fp5 human echov	474	211	10	Q9LJ33	Q9lj33 aradidopsis
402	6	3.1	191	4	Q9HAF1	Q9haf1 homo sapien	475	211	10	Q9LJ33	Q9lj33 pseudomonas
403	6	3.1	191	10	Q8LFB3	Q8lfb3 arabidopsis	476	211	10	Q9LJ33	Q9lj33 pseudomonas
404	6	3.1	191	16	Q8Y9P0	Q8y9p0 listeria mo	477	211	10	Q9LJ33	Q9lj33 pseudomonas
405	6	3.1	191	16	Q8PCQ1	Q8pcq1 xanthomonas	478	211	10	Q9LJ33	Q9lj33 pseudomonas
406	6	3.1	191	16	Q8LW93	Q8lw93 macaca fasc	479	211	10	Q9LJ33	Q9lj33 pseudomonas
407	6	3.1	192	11	Q9D7J5	Q9d7j5 mus musculu	480	211	10	Q9LJ33	Q9lj33 pseudomonas
408	6	3.1	192	11	Q9D7J5	Q9d7j5 mus musculu	481	211	10	Q9LJ33	Q9lj33 pseudomonas
409	6	3.1	192	13	Q9PW13	Q9pw13 cynops ensi	482	211	10	Q9LJ33	Q9lj33 pseudomonas
410	6	3.1	192	17	Q8TY69	Q8ty69 methanopyru	483	211	10	Q9LJ33	Q9lj33 pseudomonas
411	6	3.1	193	6	Q95KF9	Q95kf9 macaca fasc	484	211	10	Q9LJ33	Q9lj33 pseudomonas
412	6	3.1	193	16	Q8RBB9	Q8rb9 thermomanaer	485	211	10	Q9LJ33	Q9lj33 pseudomonas
413	6	3.1	194	16	Q07001	Q07001 bacillus su	486	211	10	Q9LJ33	Q9lj33 pseudomonas
414	6	3.1	195	10	Q8S2S7	Q8s2s7 theillungiel	487	211	10	Q9LJ33	Q9lj33 pseudomonas
415	6	3.1	195	17	Q97B70	Q97b70 thermoplas	488	211	10	Q9LJ33	Q9lj33 pseudomonas
416	6	3.1	196	10	Q9SWY4	Q9swy4 dunaliella	489	211	10	Q9LJ33	Q9lj33 pseudomonas
417	6	3.1	196	13	P79827	P79827 oncorhynch	490	211	10	Q9LJ33	Q9lj33 pseudomonas
418	6	3.1	196	16	Q8DGL7	Q8dgl7 synecococ	491	211	10	Q9LJ33	Q9lj33 pseudomonas
419	6	3.1	196	17	Q9HRP6	Q9hrp6 halobacteri	492	211	10	Q9LJ33	Q9lj33 pseudomonas
420	6	3.1	197	2	Q7XZ87	Q7xz87 rhizobium f	493	211	10	Q9LJ33	Q9lj33 pseudomonas
421	6	3.1	197	5	Q38872	Q38872 dictyosteli	494	211	10	Q9LJ33	Q9lj33 pseudomonas
422	6	3.1	197	16	Q9JVD7	Q9jvd7 neisseria m	495	211	10	Q9LJ33	Q9lj33 pseudomonas
423	6	3.1	197	16	Q8EDN3	Q8edn3 shewanella	496	211	10	Q9LJ33	Q9lj33 pseudomonas
424	6	3.1	197	16	Q89TGI	Q89tgi bradyrhizob	497	211	10	Q9LJ33	Q9lj33 pseudomonas
425	6	3.1	198	2	Q92B15	Q92b15 leuconostoc	498	211	10	Q9LJ33	Q9lj33 pseudomonas
426	6	3.1	198	16	Q8REB6	Q8reb6 fusobacteri	499	211	10	Q9LJ33	Q9lj33 pseudomonas
427	6	3.1	199	10	Q93386	Q93386 brassica ol	500	211	10	Q9LJ33	Q9lj33 pseudomonas
428	6	3.1	199	10	Q84JX7	Q84jx7 oryza sativ	501	211	10	Q9LJ33	Q9lj33 pseudomonas
429	6	3.1	199	16	Q8D3Q2	Q8d3q2 vibrio vuln	502	211	10	Q9LJ33	Q9lj33 pseudomonas
430	6	3.1	200	10	Q9LWR5	Q9lwr5 oryza sativ	503	211	10	Q9LJ33	Q9lj33 pseudomonas
431	6	3.1	200	10	Q8GVN7	Q8gvn7 oryza sativ	504	211	10	Q9LJ33	Q9lj33 pseudomonas
432	6	3.1	200	10	Q9FZK5	Q9fzk5 arabidopsis	505	211	10	Q9LJ33	Q9lj33 pseudomonas
433	6	3.1	200	16	Q8XE16	Q8xe16 escherichia	506	211	10	Q9LJ33	Q9lj33 pseudomonas
434	6	3.1	200	16	Q8DDT4	Q8ddt4 vibrio vuln	507	211	10	Q9LJ33	Q9lj33 pseudomonas
435	6	3.1	200	16	Q8CW04	Q8cw04 escherichia	508	211	10	Q9LJ33	Q9lj33 pseudomonas
436	6	3.1	200	16	Q83BE2	Q83be2 coxiella bu	509	211	10	Q9LJ33	Q9lj33 pseudomonas
437	6	3.1	201	2	Q9X7J0	Q9x7j0 pseudomonas	510	211	10	Q9LJ33	Q9lj33 pseudomonas
438	6	3.1	201	2	Q9K4R3	Q9k4r3 pseudomonas	511	211	10	Q9LJ33	Q9lj33 pseudomonas
439	6	3.1	201	4	Q7Z311	Q7z311 homo sapien	512	211	10	Q9LJ33	Q9lj33 pseudomonas
440	6	3.1	201	11	Q9CVP8	Q9cvp8 mus musculu	513	211	10	Q9LJ33	Q9lj33 pseudomonas
441	6	3.1	201	11	Q8BXD1	Q8bxdl mus musculu	514	211	10	Q9LJ33	Q9lj33 pseudomonas
442	6	3.1	202	16	Q8Y734	Q8y734 pseudomonas	515	211	10	Q9LJ33	Q9lj33 pseudomonas
443	6	3.1	202	16	Q85581	Q85581 synecocyst	516	211	10	Q9LJ33	Q9lj33 pseudomonas
444	6	3.1	203	16	Q83KR4	Q83kr4 shigella fl	517	211	10	Q9LJ33	Q9lj33 pseudomonas
445	6	3.1	203	16	Q83KR4	Q83kr4 shigella fl	518	211	10	Q9LJ33	Q9lj33 pseudomonas
446	6	3.1	204	16	Q7UAE8	Q7uae8 shigella fl	519	211	10	Q9LJ33	Q9lj33 pseudomonas
447	6	3.1	204	16	Q8E2Q5	Q8e2q5 streptococ	520	211	10	Q9LJ33	Q9lj33 pseudomonas
448	6	3.1	204	16	Q99XK6	Q99xk6 streptococ	521	211	10	Q9LJ33	Q9lj33 pseudomonas
449	6	3.1	205	10	Q7XZ29	Q7xz29 griffithsia	522	211	10	Q9LJ33	Q9lj33 pseudomonas
450	6	3.1	205	11	Q8BNX2	Q8bnx2 mus musculu	523	211	10	Q9LJ33	Q9lj33 pseudomonas
451	6	3.1	205	12	Q9QPF8	Q9qpf8 hepatitis e	524	211	10	Q9LJ33	Q9lj33 pseudomonas
452	6	3.1	205	16	Q97RX0	Q97rx0 streptococ	525	211	10	Q9LJ33	Q9lj33 pseudomonas
453	6	3.1	205	16	Q88NJ1	Q88nj1 pseudomonas	526	211	10	Q9LJ33	Q9lj33 pseudomonas
454	6	3.1	206	3	Q9P533	Q9p533 neurospora	527	211	10	Q9LJ33	Q9lj33 pseudomonas

528	6	3.1	226	16	Q8FTF5	Q8ftf5 corynebacte	601	6	3.1	252	5	Q9N4C7	Q9n4c7 caenorhabdi
529	6	3.1	226	17	Q59384	O59384 pyrococcus	602	6	3.1	252	10	Q9SP21	Q9sp21 boea crassi
530	6	3.1	227	16	Q8P8V9	Q8p8v9 xanthomonas	603	6	3.1	252	16	Q8FNW6	Q8fnw6 corynebacte
531	6	3.1	227	16	Q9L2G6	Q9l2g6 streptomyc	604	6	3.1	252	16	Q88YH4	Q88yh4 lactobacill
532	6	3.1	227	16	Q82B09	Q82b09 streptomyc	605	6	3.1	252	16	Q81A80	Q81a80 bacillus ce
533	6	3.1	228	10	Q9LMK7	Q9lmk7 arabidopsis	606	6	3.1	252	17	Q97A60	Q97a60 thermoplas
534	6	3.1	228	5	Q94195	Q94195 caenorhabdi	607	6	3.1	253	2	Q9X4R1	Q9x4r1 enterococc
535	6	3.1	230	16	Q88NT3	Q88nt3 pseudomonas	608	6	3.1	253	10	Q22082	Q22082 petunia hyb
536	6	3.1	231	16	Q7WK40	Q7wk40 bordetella	609	6	3.1	253	13	Q9DDF5	Q9ddf5 gallus gall
537	6	3.1	231	16	Q7W8T0	Q7w8t0 bordetella	610	6	3.1	254	16	Q97S14	Q97s14 streptococ
538	6	3.1	231	16	Q7VZ31	Q7vz31 bordetella	611	6	3.1	254	16	Q67535	Q67535 aquifex aeo
539	6	3.1	231	17	Q8U0V8	Q8u0v8 pyrococcus	612	6	3.1	256	10	Q7XKH2	Q7xkh2 oryza sativ
540	6	3.1	232	10	Q9ST20	Q9st20 brassica ca	613	6	3.1	256	11	Q7TPA6	Q7tpa6 rattus norv
541	6	3.1	232	16	Q8G5N9	Q8g5n9 bifidobacte	614	6	3.1	256	13	Q42139	Q42139 xenopus lae
542	6	3.1	232	17	Q9V1L2	Q9v1l2 pyrococcus	615	6	3.1	257	12	Q98ZP5	Q98zp5 potato viru
543	6	3.1	233	12	Q91TV2	Q91tv2 tupaia herp	616	6	3.1	257	16	Q8F6V2	Q8f6v2 leptospira
544	6	3.1	233	10	Q949U7	Q949u7 arabidopsis	617	6	3.1	258	5	Q19326	Q19326 caenorhabdi
545	6	3.1	234	10	Q04149	Q04149 arabidopsis	618	6	3.1	258	10	Q9XIC2	Q9xic2 arabidopsis
546	6	3.1	234	10	Q9XHS1	Q9xhs1 arabidopsis	619	6	3.1	258	12	Q81861	Q81861 hepatitis e
547	6	3.1	234	16	Q8K8Q7	Q8k8q7 streptococ	620	6	3.1	258	16	Q9K4B7	Q9k4b7 streptomyce
548	6	3.1	236	16	Q8RVH6	Q8rvh6 deinococcc	621	6	3.1	258	16	Q8EPP5	Q8ep5 oceanobacil
549	6	3.1	236	16	Q8F9V4	Q8f9v4 leptospira	622	6	3.1	259	10	Q7XS97	Q7xs97 oryza sativ
550	6	3.1	236	16	Q7U4E2	Q7u4e2 synecococc	623	6	3.1	260	11	Q8CEW5	Q8cew5 mus musculu
551	6	3.1	237	7	Q31466	Q31466 morone saxa	624	6	3.1	260	11	Q8BMX8	Q8bm8 mus musculu
552	6	3.1	237	10	Q9LUC7	Q9luc7 arabidopsis	625	6	3.1	260	16	Q9KRC5	Q9kr5 vibrio chol
553	6	3.1	238	5	Q8STH9	Q8st9 encephalito	626	6	3.1	260	16	Q9HYV6	Q9hyv6 pseudomonas
554	6	3.1	238	16	Q7WGZ9	Q7wz9 bordetella	627	6	3.1	262	10	Q9M3C1	Q9m3c1 arabidopsis
555	6	3.1	238	16	Q7W9Q9	Q7w9q9 bordetella	628	6	3.1	262	16	Q8X8R8	Q8x8r8 escherichia
556	6	3.1	238	16	Q7VWB7	Q7vw7 bordetella	629	6	3.1	262	16	Q7UVY7	Q7uvy7 rhodopirell
557	6	3.1	238	17	Q8TJK7	Q8tjk7 methanosarc	630	6	3.1	262	2	Q7X3Q9	Q7x3q9 staphylococ
558	6	3.1	239	5	Q9VIU0	Q9viu0 drosophila	631	6	3.1	263	5	Q9GUD6	Q9gud6 habesia big
559	6	3.1	239	10	Q8LA42	Q8la42 arabidopsis	632	6	3.1	263	5	Q9GNT5	Q9gni5 habesia big
560	6	3.1	239	10	Q8H5V6	Q8h5v6 oryza sativ	633	6	3.1	263	13	Q803P1	Q803p1 brachydanio
561	6	3.1	239	16	Q89S00	Q89s0 clostridium	634	6	3.1	264	16	Q87QW5	Q87qw5 vibrio para
562	6	3.1	239	16	Q82BT0	Q82bt0 streptomyc	635	6	3.1	264	11	Q8BWM4	Q8bwm4 mus musculu
563	6	3.1	240	4	Q8TED2	Q8ted2 homo sapien	636	6	3.1	264	16	Q9RUN3	Q9run3 deinococcus
564	6	3.1	240	16	Q8R9H7	Q8r9h7 thermococcc	637	6	3.1	264	16	Q8CWT1	Q8cwt1 streptococ
565	6	3.1	240	16	Q8P2R5	Q8p2r5 streptococ	638	6	3.1	265	2	Q9AMZ4	Q9amz4 bradyrhizob
566	6	3.1	241	4	Q9NP64	Q9np64 homo sapien	639	6	3.1	265	5	P90819	P90819 caenorhabdi
567	6	3.1	241	11	Q9ESX4	Q9esx4 mus musculu	640	6	3.1	265	5	P90819	P90819 streptococ
568	6	3.1	241	17	Q8TNU5	Q8tnu5 methanosarc	641	6	3.1	266	2	Q93MY2	Q93my2 streptococ
569	6	3.1	242	13	Q9YH13	Q9yh13 gallus gall	642	6	3.1	266	3	Q42898	Q42898 schizosacch
570	6	3.1	242	13	Q7ZV17	Q7zv17 brachydanio	643	6	3.1	266	3	Q42898	Q42898 schizosacch
571	6	3.1	242	17	Q9HLV4	Q9hlv4 thermoplas	644	6	3.1	267	5	Q86DV4	Q86dv4 schistosoma
572	6	3.1	243	11	Q9CTE2	Q9ct2 mus musculu	645	6	3.1	267	5	Q86DV4	Q86dv4 schistosoma
573	6	3.1	243	16	Q69830	Q69830 streptomyc	646	6	3.1	267	5	Q9BDK9	Q9bd9 sus scrofa
574	6	3.1	244	16	Q7U4R3	Q7u4r3 synecococc	647	6	3.1	267	10	Q9MSU2	Q9msu2 arabidopsis
575	6	3.1	245	2	Q31394	Q31394 bacillus me	648	6	3.1	267	10	Q9MSU2	Q9msu2 arabidopsis
576	6	3.1	245	16	Q9KUE6	Q9kue6 vibrio chol	649	6	3.1	267	12	Q9LH75	Q9lh75 cherry necr
577	6	3.1	245	16	Q8KEM0	Q8kemo chlorobium	650	6	3.1	267	13	Q9PUV0	Q9puv0 balistes sp
578	6	3.1	245	16	Q8F4X1	Q8f4x1 leptospira	651	6	3.1	267	13	Q9PUV0	Q9puv0 balistes sp
579	6	3.1	245	16	Q8F4X1	Q8f4x1 leptospira	652	6	3.1	267	16	Q8DT65	Q8dt65 streptococ
580	6	3.1	246	2	Q83043	Q83043 azospirillu	653	6	3.1	268	9	Q8SDW2	Q8sdw2 bacterioph
581	6	3.1	246	2	Q9F7F1	Q9f7f1 azospirillu	654	6	3.1	268	9	Q8SDW2	Q8sdw2 bacterioph
582	6	3.1	246	5	Q9BHA3	Q9bha3 sabelia spa	655	6	3.1	269	2	Q8KLS6	Q8kl56 rhodobacter
583	6	3.1	247	10	Q84TE5	Q84te5 arabidopsis	656	6	3.1	269	2	Q8KLS6	Q8kl56 rhodobacter
584	6	3.1	247	16	Q7WH87	Q7wh87 bordetella	657	6	3.1	269	2	Q9RCK9	Q9rcck9 caenorhabdi
585	6	3.1	247	16	Q7W9H5	Q7w9h5 bordetella	658	6	3.1	269	5	Q22638	Q22638 caenorhabdi
586	6	3.1	248	5	Q81S06	Q81s06 bugia mala	659	6	3.1	269	5	Q22638	Q22638 caenorhabdi
587	6	3.1	248	12	Q81860	Q81860 hepatitis e	660	6	3.1	269	10	Q39647	Q39647 cucurbita c
588	6	3.1	248	17	Q9PUW2	Q9puw2 methanosarc	661	6	3.1	269	16	Q9RCS5	Q9rcs5 streptococ
589	6	3.1	249	10	Q7X9H6	Q7x9h6 arabidopsis	662	6	3.1	269	16	Q9RCS5	Q9rcs5 streptococ
590	6	3.1	249	13	Q7SXU0	Q7sxu0 brachydanio	663	6	3.1	269	16	Q8RBS9	Q8res9 fusobacteri
591	6	3.1	249	16	Q97HF0	Q97hf0 clostridium	664	6	3.1	269	16	Q8RBS9	Q8res9 fusobacteri
592	6	3.1	249	16	Q97HF0	Q97hf0 clostridium	665	6	3.1	269	16	Q8RBS9	Q8res9 fusobacteri
593	6	3.1	249	16	Q25574	Q25574 helicobacte	666	6	3.1	269	16	Q8RBS9	Q8res9 fusobacteri
594	6	3.1	250	5	P90779	P90779 bruceella su	667	6	3.1	269	16	Q8RBS9	Q8res9 fusobacteri
595	6	3.1	250	10	Q9LMV5	Q9lmv5 arabidopsis	668	6	3.1	270	2	Q9RCK9	Q9rcck9 caenorhabdi
596	6	3.1	250	16	Q8EPK7	Q8epk7 oceanobacil	669	6	3.1	270	2	Q9RCK9	Q9rcck9 caenorhabdi
597	6	3.1	250	16	Q8ZNE4	Q8zne4 streptomyc	670	6	3.1	270	2	Q9RCK9	Q9rcck9 caenorhabdi
598	6	3.1	251	2	Q9RMN8	Q9rmn8 neisseria m	671	6	3.1	270	2	Q9RCK9	Q9rcck9 caenorhabdi
599	6	3.1	251	2	Q9RMN8	Q9rmn8 neisseria m	672	6	3.1	270	2	Q9RCK9	Q9rcck9 caenorhabdi
600	6	3.1	251	10	Q9LI72	Q9li72 arabidopsis	673	6	3.1	270	2	Q9RCK9	Q9rcck9 caenorhabdi

674	6	3.1	281	16	Q9CKM7	Q9ckm7 pasteurella	747	6	3.1	302	10	Q22066	Q22066 arabidopsis
675	6	3.1	282	2	Q9R6G8	Q9r6g8 agrobacteri	748	6	3.1	302	10	Q8LP01	Q8lp01 arabis gemm
676	6	3.1	282	5	Q9GUD5	Q9gud5 babesia big	749	6	3.1	302	10	Q22072	Q22072 arabidopsis
677	6	3.1	282	5	Q9GUD2	Q9gud2 babesia big	750	6	3.1	302	10	Q22068	Q22068 arabidopsis
678	6	3.1	282	5	Q9GUD4	Q9gud4 babesia big	751	6	3.1	302	10	Q22065	Q22065 arabidopsis
679	6	3.1	282	5	Q9GUD3	Q9gud3 babesia big	752	6	3.1	302	10	Q8LP04	Q8lp04 arabis gemm
680	6	3.1	282	5	Q9GUD8	Q9gud8 babesia big	753	6	3.1	302	10	Q8LP08	Q8lp08 arabis gemm
681	6	3.1	282	5	Q9L5708	Q9l5708 babesia big	754	6	3.1	302	10	Q22074	Q22074 arabis gemm
682	6	3.1	283	2	Q05342	Q05342 versinia ps	755	6	3.1	302	10	Q22074	Q22074 arabis gemm
683	6	3.1	283	10	Q81802	Q81802 arabidopsis	756	6	3.1	302	10	Q8LP02	Q8lp02 arabis gemm
684	6	3.1	283	16	Q988E7	Q988e7 rhizobium l	757	6	3.1	302	10	Q8LP06	Q8lp06 arabidopsis
685	6	3.1	283	16	Q9RJF9	Q9rjf9 streptomyce	758	6	3.1	302	10	Q22075	Q22075 arabis glab
686	6	3.1	284	10	Q40595	Q40595 nicotiana t	759	6	3.1	302	10	Q22069	Q22069 arabidopsis
687	6	3.1	285	16	Q97DX1	Q97dx1 clostridium	760	6	3.1	302	10	Q22067	Q22067 arabidopsis
688	6	3.1	285	16	Q2L0X4	Q2l0x4 streptomyce	761	6	3.1	302	16	Q7WF30	Q7wf30 bordetella
689	6	3.1	285	16	Q8DVP2	Q8dvp2 streptococc	762	6	3.1	302	16	Q7W3Q3	Q7w3q3 bordetella
690	6	3.1	286	5	Q9GQS1	Q9gqs1 meloidogyne	763	6	3.1	302	16	Q7VST9	Q7vst9 bordetella
691	6	3.1	286	10	Q8W507	Q8w507 nicotiana t	764	6	3.1	302	16	Q7U653	Q7u653 synchococc
692	6	3.1	286	10	Q81013	Q81013 arabidopsis	765	6	3.1	303	10	Q64761	Q64761 arabidopsis
693	6	3.1	286	10	Q9LYV1	Q9lyv1 arabidopsis	766	6	3.1	303	10	Q55483	Q55483 synchocyst
694	6	3.1	286	16	Q9ZL77	Q9zl77 helicobacte	767	6	3.1	303	16	Q8NTU5	Q8ntus corynebacte
695	6	3.1	287	10	Q8LEK3	Q8lek3 arabidopsis	768	6	3.1	305	16	Q82LI5	Q82li5 streptomyce
696	6	3.1	287	10	Q09224	Q09224 nicotiana e	769	6	3.1	305	16	Q7Z0G8	Q7z0g8 metapenaeus
697	6	3.1	287	10	Q9LTX3	Q9ltx3 arabidopsis	770	6	3.1	306	5	Q8C742	Q8c742 mus musculu
698	6	3.1	288	2	Q9AKE5	Q9ake5 rickettsia	771	6	3.1	306	16	Q8XA42	Q8xa42 escherichia
699	6	3.1	288	8	Q35993	Q35993 trypanosoma	772	6	3.1	306	16	Q8XVC8	Q8xvc8 ralstonia s
700	6	3.1	288	10	Q9XGF4	Q9xgf4 solanum tub	773	6	3.1	306	16	Q8FF21	Q8ff21 escherichia
701	6	3.1	288	10	Q23771	Q23771 cratereostig	774	6	3.1	306	16	Q83K34	Q83k34 shigella fl
702	6	3.1	289	10	Q23272	Q23272 arabidopsis	775	6	3.1	307	10	Q94JVS	Q94jvs arabidopsis
703	6	3.1	289	10	Q38911	Q38911 arabidopsis	776	6	3.1	307	16	Q89HT1	Q89ht1 bradyrhizob
704	6	3.1	289	12	Q9YILL1	Q9yll1 human echov	777	6	3.1	308	2	Q93E11	Q93e11 rhizobium l
705	6	3.1	289	16	Q81X64	Q81x64 bacillus an	778	6	3.1	309	5	Q9VED5	Q9ved5 drosophila
706	6	3.1	289	17	Q96ZX0	Q96zx0 sulfolobus	779	6	3.1	309	5	Q81GM9	Q81gm9 nitrophila
707	6	3.1	290	2	Q9AQX4	Q9aqx4 rickettsia	780	6	3.1	309	16	Q82VX5	Q82vx5 drosophila
708	6	3.1	290	2	Q9AKX0	Q9akx0 rickettsia	781	6	3.1	310	16	Q8ENQ7	Q8enq7 oceanobacil
709	6	3.1	290	12	Q8B912	Q8b912 racchipusia	782	6	3.1	310	16	Q59456	Q59456 halobacteri
710	6	3.1	291	10	Q8LG58	Q8lg58 arabidopsis	783	6	3.1	312	2	P72457	P72457 streptomyce
711	6	3.1	291	10	Q9LK45	Q9lk45 arabidopsis	784	6	3.1	312	16	Q26068	Q26068 helicobacte
712	6	3.1	291	10	Q7XZP8	Q7xzp8 oryza sativ	785	6	3.1	312	16	Q67040	Q67040 aquifex aeo
713	6	3.1	291	17	Q8RYSO	Q8ryso methanopyru	786	6	3.1	312	16	Q9ZJ59	Q9zj59 helicobacte
714	6	3.1	292	10	Q8GRL4	Q8grl4 oryza sativ	787	6	3.1	312	16	Q7U4U4	Q7u4u4 shigella fl
715	6	3.1	292	11	Q7TQ94	Q7tq94 rattus norv	788	6	3.1	312	17	Q9HQK0	Q9hqk0 halobacteri
716	6	3.1	293	10	Q49876	Q49876 lupinus alb	789	6	3.1	313	4	Q9UKA0	Q9uka0 homo sapien
717	6	3.1	294	5	Q9W0A9	Q9w0a9 drosophila	790	6	3.1	314	16	Q82FY5	Q82fy5 streptomyce
718	6	3.1	294	16	Q7W5M2	Q7w5m2 bordetella	791	6	3.1	314	5	Q20123	Q20123 caenorhabdi
719	6	3.1	294	16	Q7VW63	Q7vw63 bordetella	792	6	3.1	315	16	Q8ZGD8	Q8zgd8 yerinia pe
720	6	3.1	295	2	Q66147	Q66147 plectonema	793	6	3.1	315	16	Q9LE50	Q9le50 arabidopsis
721	6	3.1	295	10	Q8LP08	Q8lp08 crucihmala	794	6	3.1	316	10	Q9HXK2	Q9hxx2 pseudomonas
722	6	3.1	295	10	Q8LP05	Q8lp05 crucihmala	795	6	3.1	316	16	Q8RC66	Q8rc66 thermoaer
723	6	3.1	295	10	Q8LP07	Q8lp07 olimarabido	796	6	3.1	316	16	Q8RC66	Q8rc66 thermoaer
724	6	3.1	296	16	Q8XEM0	Q8xem0 ralstonia s	797	6	3.1	317	16	Q7VGP1	Q7vgp1 helicobacte
725	6	3.1	297	16	Q8UA53	Q8ua53 agrobacteri	798	6	3.1	318	16	Q9JNS5	Q9jns5 neisseria m
726	6	3.1	298	4	Q75628	Q75628 homo sapien	799	6	3.1	318	16	Q8F9Q7	Q8f9q7 leptospira
727	6	3.1	298	4	Q9NP57	Q9np57 homo sapien	800	6	3.1	319	16	Q92PG1	Q92pg1 rhizobium m
728	6	3.1	298	10	Q9SXM5	Q9sxm5 glycine max	801	6	3.1	320	4	Q8N4Q3	Q8n4q3 homo sapien
729	6	3.1	298	10	Q9XGB4	Q9xgb4 trifolium r	802	6	3.1	320	17	Q8ZT08	Q8zt08 pyrobaculum
730	6	3.1	298	16	Q8PDI3	Q8pd13 xanthomonas	803	6	3.1	321	2	Q9XCZ6	Q9xcz6 pseudomonas
731	6	3.1	298	16	Q86B08	Q86b08 pseudomonas	804	6	3.1	321	2	Q9XCZ3	Q9xcz3 pseudomonas
732	6	3.1	299	10	Q9S7G9	Q9s7g9 glycine max	805	6	3.1	321	5	Q867V1	Q867v1 drosophila
733	6	3.1	299	10	Q9S7G9	Q9s7g9 glycine max	806	6	3.1	321	16	Q83CU5	Q83cu5 coxiella bu
734	6	3.1	300	11	Q8BY15	Q8by15 mus musculu	807	6	3.1	321	16	Q7WNJ8	Q7wnj8 bordetella
735	6	3.1	300	10	Q9SFG6	Q9sf6 arabidopsis	808	6	3.1	322	5	Q86C08	Q86c08 drosophila
736	6	3.1	300	11	Q8BY15	Q8by15 mus musculu	809	6	3.1	322	5	Q86C07	Q86c07 drosophila
737	6	3.1	301	11	Q8BY15	Q8by15 mus musculu	810	6	3.1	322	5	Q86C06	Q86c06 drosophila
738	6	3.1	301	11	Q8BY15	Q8by15 mus musculu	811	6	3.1	322	5	Q86C05	Q86c05 drosophila
739	6	3.1	301	16	Q83B50	Q83b50 coxiella bu	812	6	3.1	322	5	Q867Y1	Q867y1 drosophila
740	6	3.1	302	10	Q22076	Q22076 arabidopsis	813	6	3.1	322	5	Q7Z0G9	Q7z0g9 metapenaeus
741	6	3.1	302	10	Q22070	Q22070 arabidopsis	814	6	3.1	322	10	Q9AR42	Q9ar42 oryza sativ
742	6	3.1	302	10	Q8LP09	Q8lp09 arabidopsis	815	6	3.1	322	12	Q9Q6F9	Q9q6f9 grapevine l
743	6	3.1	302	10	Q22073	Q22073 arabidopsis	816	6	3.1	322	16	Q926E8	Q926e8 rhizobium m
744	6	3.1	302	10	Q8LP03	Q8lp03 arabis gemm	817	6	3.1	322	16	Q8PDR4	Q8pdr4 xanthomonas
745	6	3.1	302	10	Q8LQ09	Q8lq09 arabis gemm	818	6	3.1	323	2	Q9XCZ5	Q9xcz5 pseudomonas
746	6	3.1	302	10	Q22071	Q22071 arabidopsis	819	6	3.1	323	4	Q8N4M3	Q8n4m3 homo sapien







Ralstonia solanacearum (Pseudomonas solanacearum).  
Plasmid megaplasmid.  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Burkholderiaceae; Ralstonia.  
NCBI\_TaxID=305;  
[1]\_RN  
SEQUENCE FROM N.A.  
STRAIN=CM11000; PLASMID=megaplasmid;  
MEDLINE=21681879; PubMed=11823852;  
Salanoubat M., Genin S., Ariguenave F., Gouzy J., Mangerot S.,  
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
Chandler M., Choien N., Claudel-Renard C., Cunnac S., Denange T.,  
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,  
Weissenbach J., Boucher C.A.;  
"Genome sequence of the plant pathogen Ralstonia solanacearum.";  
Nature 415:497-502 (2002).  
EMBL; AL646084; CAD18506.1; --  
GO; GO:0046821; C:extrachromosomal DNA; IEA.  
InterPro; IPR000437; Prok\_lipoprotein S.  
PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
Plasmid; Complete proteome.  
SEQUENCE 321 AA; 35873 MW; 3308627C7C538AAD CRC64;  
SQ  
Query Match 4.1%; Score 8; DB 16; Length 321;  
Best Local Similarity 100.0%; Pred. No. 9.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 SLGGGLAQ 20  
| | | | |  
DB 198 SLGGGLAQ 205  
| | | | |  
RESULT 4  
Q82B38 PRELIMINARY; PRT; 484 AA.  
ID Q82B38  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative transmembrane transport protein.  
GN SAV5867.  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
"Genome sequence of an industrial microorganism Streptomyces  
avermitilis: deducing the ability of producing secondary  
metabolites.";  
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
"Genome sequence of an industrial microorganism Streptomyces  
avermitilis: deducing the ability of producing secondary  
metabolites.";  
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
Sakaki Y., Hattori M., Omura S.;  
"Complete genome sequence and comparative analysis of the industrial  
microorganism Streptomyces avermitilis.";  
Nat. Biotechnol. 21:526-531 (2003).  
DR EMBL; AP005044; BAC73579.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR004638; E:flux\_EmrB.  
DR InterPro; IPR007114; MFS.  
DR InterPro; IPR000437; Prok\_lipoprot\_S.

DR TIGRFAMs; TIGR00711; efflux\_EmrB; 1.  
DR PROSITE; PS50850; MFS; 1.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Transmembrane; Complete proteome.  
SQ SEQUENCE 484 AA; 48820 MW; AFCBF0EB99CD415 CRC64;  
[1]\_RN  
Query Match 4.1%; Score 8; DB 16; Length 484;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 SLGGGLAQ 20  
| | | | |  
DB 105 SLGGGLAQ 112  
| | | | |  
RESULT 5  
Q9L004 PRELIMINARY; PRT; 489 AA.  
ID Q9L004  
AC Q9L004;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative transmembrane transport protein.  
GN SCO3309 OR SCC30.17C.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Seeger K.J., Harris D.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,  
Kinashi H., Hopwood D.A.;  
"A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
Mol. Microbiol. 21:77-96 (1996).  
[4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,  
Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,  
Hopwood D.A.;  
"Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";  
Nature 417:141-147 (2002).  
RL EMBL; AL939112; CAB88187.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR004638; E:flux\_EmrB.  
DR InterPro; IPR007114; MFS.  
DR InterPro; IPR005828; Sub\_transporter.  
DR Pfam; PF00083; sugar\_tr; 1.  
DR TIGRFAMs; TIGR00711; efflux\_EmrB; 1.  
DR PROSITE; PS50850; MFS; 1.

Transmembrane; Complete proteome.  
 SEQUENCE 489 AA; 49197 MW; C8013FC0B232E52F CRC64;  
 Query Match 4.1%; Score 8; DB 16; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 SGGGLAQ 20  
 |||||  
 Db 107 SGGGLAQ 114  
 |||||  
 RESULT 6  
 Q7WL74 PRELIMINARY; PRT; 497 AA.  
 ID Q7WL74  
 AC Q7WL74;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Putative aldehyde dehydrogenase.  
 GN BB1875.  
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 NCBI\_TaxID=518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RB50 / ATCC BAA-588;  
 RX MEDLINE=22827954; PubMed=12910271;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,  
 Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,  
 Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
 Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
 Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
 "Comparative analysis of the genome sequences of Bordetella pertussis,  
 Bordetella parapertussis and Bordetella bronchiseptica.";  
 Nat. Genet. 35:32-40(2003).  
 DR EMBL; BX640442; CAE32372.1; --  
 KW Complete proteome.  
 SQ SEQUENCE 497 AA; 53676 MW; D2F05173AA568403 CRC64;  
 Query Match 4.1%; Score 8; DB 16; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 150 FVSKVEAC 157  
 |||||  
 Db 318 FVSKVEAC 325  
 |||||  
 RESULT 7  
 Q7WT74 PRELIMINARY; PRT; 497 AA.  
 ID Q7WT74  
 AC Q7WT74;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Putative aldehyde dehydrogenase.  
 GN BPP2426.  
 OS Bordetella parapertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 NCBI\_TaxID=519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=12822 / ATCC BAA-587;  
 RX MEDLINE=22827954; PubMed=12910271;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,  
 Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
 Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
 Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
 "Comparative analysis of the genome sequences of Bordetella pertussis,  
 Bordetella parapertussis and Bordetella bronchiseptica.";  
 Nat. Genet. 35:32-40(2003).  
 DR EMBL; BX640430; CAE37722.1; --  
 KW Complete proteome.  
 SQ SEQUENCE 497 AA; 53676 MW; D2F05173AA568403 CRC64;

Query Match 4.1%; Score 8; DB 16; Length 497;

Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 FVSKVEAC 157

|||||

Db 318 FVSKVEAC 325

|||||

RESULT 8

Q7VWF4

ID Q7VWF4 PRELIMINARY; PRT; 497 AA.

AC Q7VWF4;

DT 01-OCT-2003 (TREMBlrel. 25, Created)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Putative aldehyde dehydrogenase.

GN BP2303.

OS Bordetella pertussis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Alcaligenaceae; Bordetella.

NCBI\_TaxID=520;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

RX MEDLINE=22827954; PubMed=12910271;

RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).

DR EMBL; BX640417; CAE42576.1; --

KW Complete proteome.

SQ SEQUENCE 497 AA; 53633 MW; E84BE6B75ED9B0EB CRC64;

Query Match 4.1%; Score 8; DB 16; Length 497;

Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 FVSKVEAC 157

|||||

Db 318 FVSKVEAC 325

|||||

RESULT 9

Q9C6J7

ID Q9C6J7 PRELIMINARY; PRT; 528 AA.

AC Q9C6J7;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

```

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003959; AAA_Alipase_Centr.
DR InterPro; IPR003960; AAA_sub.
DR InterPro; IPR000642; Peptidase_M41.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF01434; Peptidase_M41; 1.
DR PROSITE; PS00674; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 603 AA; 67184 MW; A2DE7D2C930AAE23 CRC64;

Query Match 4.1%; Score 8; DB 16; Length 603;
Best Local Similarity 100.0%; Pred.No.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AEEKEEL 194
DB 166 AEEKEEL 173

RESULT 11
QY815 PRELIMINARY; PRT; 637 AA.
AC Q9Y815;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical C2H2 zinc finger protein.
GN SPBC1105.14.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972b-1.
RA McDougall R.C., Rajandream M.A., Barrell B.G., Rampsperger U.,
RA Bothe G., Fohl T.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL096851; CAB50977.1; -.
DR PIR; T39291; T39291.
DR GenedB SPombe; SPBC1105.14; -.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 637 AA; 69079 MW; C63CA05E448624AE CRC64;

Query Match 4.1%; Score 8; DB 3; Length 637;
Best Local Similarity 100.0%; Pred.No.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 SDLKRSIG 149
DB 279 SDLKRSIG 286

RESULT 12
QY815 PRELIMINARY; PRT; 768 AA.
AC Q9C6J6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN F8A12.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

```

## SEQUENCE FROM N.A.

STRAIN=CV. Columbia;  
MEDLINE=21016719; PubMed=1130712;  
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,  
Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,  
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
"Sequence and analysis of chromosome 1 of the plant Arabidopsis  
thaliana";  
Nature 408:816-820(2000).  
EMBL; AC079284; AAG50939.1; -.  
PIR; C96545; C96545.  
Hypothetical protein.  
SEQUENCE 768 AA; 88414 MW; F52E5065B2BA23AA CRC64;

Query Match 4.1%; Score 8; DB 10; Length 768;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## 7 FLVLWLSL 14

|||||  
214 FLVLWLSL 221

## RESULT 13

D Q80X16 PRELIMINARY; PRT; 5035 AA.

01-JUN-2003 (TrEMBLrel. 24, Created)

01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

RyR1.

Mus musculus (Mouse).

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

SEQUENCE FROM N.A.

STRAIN=BALB/cx3D-1F1;

Kraev A., Kraev N., MacLennan D.H.;

"Complete transcript sequence and strain-specific polymorphisms of the

Ryrl gene of the house mouse";

Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

EMBL; AY268935; AAF29981.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005262; F:calcium channel activity; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006816; P:calcium ion transport; IEA.

GO; GO:0006812; P:calcium transport; IEA.

InterPro; IPR000699; Ca-rel\_channel.

InterPro; IPR01682; Ca/Na pore.

InterPro; IPR02048; EF-hand.

InterPro; IPR005821; Ion trans.

InterPro; IPR003608; MIR.

InterPro; IPR01215; Ryanodn\_receptor.

InterPro; IPR003032; RyR.

InterPro; IPR003877; SPRY\_receptor.

Pfam; PF00520; ion trans; 1.

Pfam; PF02815; MIR; 3.

DR Pfam; PF01365; RYDR\_ITPR; 2.

DR Pfam; PF02026; RYR; 4.

DR Pfam; PF00622; SPRY; 3.

DR PRINTS; PR00795; RYANODINER.

DR SMART; SM00472; MIR; 4.

DR SMART; SM00449; SPRY; 3.

KW Receptor.

SQ SEQUENCE 5035 AA; 565034 MW; D590990FA5846B76 CRC64;

Query Match 4.1%; Score 8; DB 11; Length 5035;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 187 AEEKEEL 194

|||||

Db 1916 AEEKEEL 1923

## RESULT 14

Q984N0 PRELIMINARY; PRT; 49 AA.

AC Q984N0;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical protein msr7929.

GN MSR7929.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI\_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RA MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic bacterium

Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL; AP003013; BAB53599.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 49 AA; 5601 MW; 64D3E860FIADC82B CRC64;

Query Match 3.6%; Score 7; DB 16; Length 49;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 53 FLELLGG 59

|||||

Db 26 FLELLGG 32

## RESULT 15

Q8YMR5 PRELIMINARY; PRT; 63 AA.

AC Q8YMR5;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein Asl4865.

GN Asl4865.

OS Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI\_TaxID=103690;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21595285; PubMed=11759840;

RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,  
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,  
RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
RL cyanobacterium Anabaena sp. strain PCC 7120.";  
RL DNA Res. 8:205-213(2001).  
DR EMBL; AP003597; BAB76564.1; --  
DR PIR; A12413; A12413.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 63 AA; 7615 MW; E86A0688CE22DE79 CRC64;

Query Match 3.6%; Score 7; DB 16; Length 63;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 91 YFLGLKV 97  
|||  
Db 54 YFLGLKV 60

Search completed: May 17, 2004, 10:53:00  
Job time : 86 secs